14, Appl 14, Appl 2, Appli 2, Appli 1, Appli

17, Appl 17, Appl 18, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl 11, Appl 11, Appl 11, Appl 11, Appl

Appli

Perfect score: Sequence: Scoring table:

Searched:

OM protein

Run on:

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Sequence 1, Appli
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Patent No. 5200327
Sequence 7, Appli
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Sequence 9, Appli
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Patent No. 5518885
GENERAL INFORMATION:
APPLICANT: RAZIUDDIN
APPLICANT: SARKAR, FAZLUL H
ITILE OF INVENTION: BRBB2 PROMOTER BINDING PROTEIN IN
ITILE OF INVENTION:
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
US-09-146-283-3

US-08-579-823A-3

US-08-229-515A-14

US-08-645-865-14

US-08-422-138-2

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US-08-658-883B-1

US-09-676-610B-26

US-09-670-630-706-3

US-09-670-706-3

US-09-670-706-3

US-09-670-708-8

US-09-670-708-8

US-09-867-521-1

US-09-87-923A-1

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US-09-67-783-1
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US-08-318-193-9
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ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19 APR 1994
CLASSIFICATION: 435
TORNEVARIAN
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NAME: PERRYMAN, DAVID G
REGIEGRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPRY 404-688-9880
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                       - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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3783
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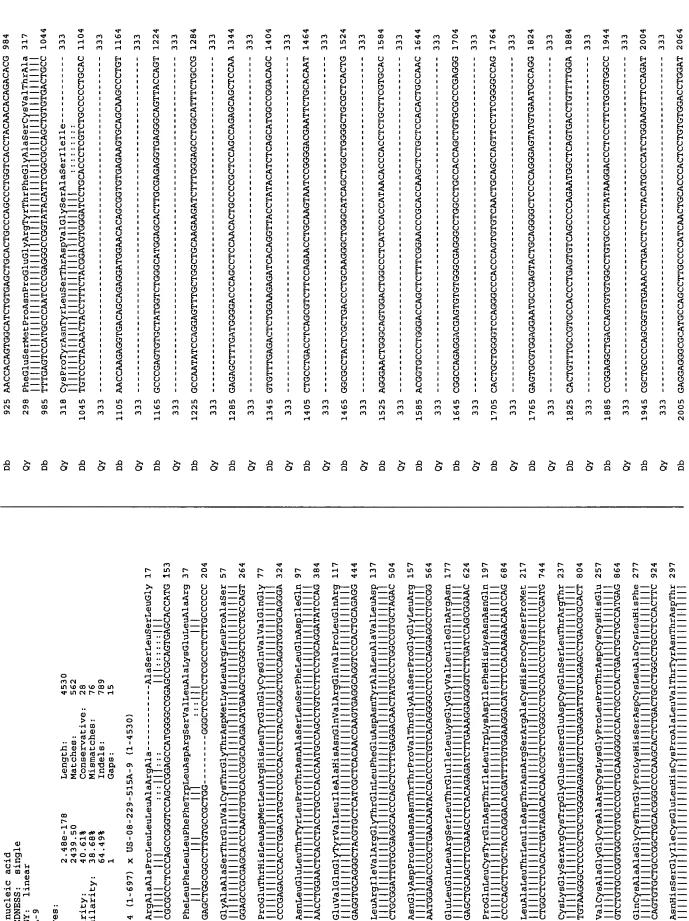
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Page 2

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i o i	TYPE: nucleic acid	g ;	925 AACCACAGIGGCAICIGIGAGCIGCACIG
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qq	205 GGAGCCGCGAGCACCCAAGTGTGCACCGGCACAAGACATGAAGCTGCCGGCCCCTGCCAGT 264	g è	1285 GAGAGCITIGAIGGGGACCCAGCCICCAA
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r 8	GAGCTGCAGCTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGTCTTGATCCAGGGAAC	qa ,	1645 CGGCCAGAGGACGAGTGTGGGGCGAGGG
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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#### ALIGNMENTS

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Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930404N10 product:v-erb-b2 erythroblastic lenkemia viral oncogene homolog 2, neuro/glioblastoma derived AK031099

ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

AK031099.1 GI:26082143 HTC; CAP trapper. Wus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

N

TITLE JOURNAL MEDLINE

PUBMED REFERENCE

AUTHORS

AUTHORS

PUBMED REFERENCE

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REFERENCE AUTHORS

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TITLE

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B. daachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoko, T., Hiraoka, T., Hiraoka, T., Hayatsu, M., Hiraoka, T., Hiraoka, T., Hiraoka, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Itoh, M., Kagawa, I., Kasukawa, T., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, M., Mushi, K., Nomura, K., Numazaki, R., Ohno, M., Ohaco, M., Nakamura, M., Saaki, C., Sakai, K., Sakai, C., Sakai, C., Sakai, Y., Sano, H., Saaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, R., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission

L. Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Genome Exploration Research Group, RIKEN Genome Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegger.riken.go.jp, Tex:81-45-503-922, Pax:81-45-503-9212,
                                                                                                                                                                                                       Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length conNa Nature 420, 563-573 (2002)

Nature 420, 563-573 (2002)
             Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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URL.http://ganome.gsc.riken.go.jp/
URL.http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                      cloning
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/mol_type="mRNA"
/strain="C57BL/6J"
                                                        Carninci, P. and Hayashizaki, Y.
High efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                  v-erb-b2 erythroblastic leukemia viral oncogene hom
neuro/glioblastoma derived oncogene homolog (avian)
(MGD|MGI:95410, GB|U71126, evidence: BLASTN, 99%,
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731
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Matches:
Conservative:
Mismatches:
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Sequence 125, App Sequence 119, App Sequence 1, Appli

Title: Perfect score:

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Sequence 124, App
Sequence 131, App
Sequence 27, Appl
Sequence 595, Appl
Sequence 10, Appl
Sequence 59, Appl
Sequence 5, Appl
Sequence 10896, A
Sequence 132, Appl
Sequence 44, Appl
Sequence 44, Appl
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Sequence 1, Appli
Sequence 8, Appli
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Sequence 45, Appli
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APPLICANT: Vidovic, Damir
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Cenpositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REPRENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 2091
US-09-821-883-9
US-09-812-883-6
US-09-812-883-6
US-09-812-883-6
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US-09-812-883-6
US-09-812-883-10
US-09-817-177-11
US-09-817-177-11
US-09-817-177-11
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US-10-116-275-131
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US-09-854-356-11
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: HER500*-rGM-CSF construct
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Patent No. US20020061310A1
GENERAL INFORMATION:
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   GenCore version 5.1.6
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Ygapop 10.0 , Ygapext
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Score

Sequence 3, Sequence 9, Sequence 5, Sequence 24, N

US-09-821-883-9				<b>q</b> 0	901 ATGCCCAATCCCGAGG
••		 		ò a	321 AsnTyrLeuSerThrA 
ity:				8 8	341 GlyGlyMetValHisH 
x (269-	3-9	.2091}		g &	1021 GGGGGCAIGGICLACC
MetArgAlaAlaP            prgsgsgcrgCaC	roleuleuleullalre	Leugl	eleuPhe	7 AG	
LeuLeuPhePheT	rpLeuAspArgSerVa]	euAlaLysGluLeuAlaArgG	g_5	ò a	381 GlyalaGlySerAspv                1141 GGGCTGGCTCCGATG
CTGCTTTTTTTCT	GGCTAGACCGAAGTGTV Y8ThrGlyThrAspMet	TAGCCAAGGAGTTGGCGCGCC ysbeuArgbeuProAlaSerF	า น—	ò d	401 SerLeuProThrHisA              1201 AGCTTCCCACACATG
_8_	GCACCGCCACAGACATO	AGCTGCGGCTCCCTGCCAGTC	CCGAGACC 180	8 8	
თ — ე	euargHisLeuTyrGlı                rcccccctctacca	slycysglnvalvalglnglyA                   gcrgccaggrggrgcaggaa	AsnLeuGlu 80            ACCTGGAA 240	qa ,	
ThrTyrL	roThrAsnAlaSerLe	serPheLeuGlnAspileGlnG		<u>8</u>	441 VAIABNGINFICABDV
CTCACCTACCTGC GlyTyrValLeuI	CCACCAATGCCAGCCTC lealaHisAsnGlnVa	CCTTCCTGCAGGATATCCAGG ArgGlnValProLeuGlnArgL		λ dd	461 AlaArgProAlaGlyA             1381 GCCCGACCTGCTGGTG
GGCTACGTGCTCA	TCGCTCACAACCAAGT	AGGCAGGTCCCACTGCAGAGGC		8	
valargglythrg 	InLeuPheGluAspAsi 	lyralaLeuAlaValLeuAspA 		g &	1441 GTCGTCAAAGACGTTT 501 GlnGlvGlvAlaalaA
ProLeuAsnAsnT              CCGCTGAACAATA	hrThrProValThrGl)	AlaSerProGlyGlyLeuArgC 	3luLeuGln 160           3AGCTGCAG 480	ව ව	CAGGGAGGAGG
LeuArgSerLeuT	hrGluIleLeuLysGl)	31yValLeuIleGlnArgAsnE		රු සි	521 LeuTyrTyrTrpAspG 
ĊİTCGAAĞCCTCA CysTyrGlnAspT	CAGAGATCTTGAAAGG hrileLeuTrpLysAsj	3GGGTCTTGATCCAGCGGAACC 11ePheHisLysAsnAsnGlnI		λo 1	
				a &	1621 ACACCTACGGCAGAGA 561 ArgSerProAsnProV
ThrLeuIleAspT              ACACTGATAGACA	hrasnargSerargali                   ccaaccgcrcrcGGGC	CysHisProCysSerProMet( 	CysLysGly 220           GTAAGGGC 660	οg	CGCTCACCCA
SerArgCysTrpG 	1. VG1uSerSerG1uAsi		24	 ₩	581 SerLeuLeuAsnAspM
GlyGlyCysAlaA	rgCysLysGlyProLe	ProThrAspCysCysHisGluC		& g	601 SerAsnGluPheSerI 
	:GCTGCAAGGGGCCACT :lyProlysHisSerAs;	SCCACTGACTGCTGCCATGAGG SystemAlaCystemHisPheA	5 ä:	ð í	621
GCCGGCTGCACGG			 AACCACAGT 840	8 8	1861 CAGGGICTACGGGGCA 641 TyrGlnThrAsnCysP
Gly11eCysGluL 	euHisCysProAlaLe	/alThrTyrAsnThrAspThrE		. 점	
GGCATCIGIGAGO Met ProAsnProG	TGCACIGCCCAGCCCLY luGlyArgTyrThrPh	3lyAlaSerCysValThrAla(		ò	661 GluaspPhelleLysA
	Alignment Scores:     Pred. No.:     Pred. No.:     Percent Similarity:     Pe	rrity: 100.00\$ matche 100.00\$ minarity: 100.00.00\$ minarity: 100.00\$ minarity: 100.00\$ minarity: 100.00\$ minarity: 100.00\$ minarity: 100.00\$ minarity: 100.00\$ minarity: 100.0	13783.00   Matches   697   Manatches   6	100.004	100.004

AspValGlySerAlaSerIleIleAsnPheGluLysLeuGlyAla 340 1080 1140 1200 1320 ValargProGlnProbroSerProArgGluGlyProLeuProAla 460 PheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrPro 500 ProglinprohisproproprohlapheSerproalapheAspAsn 520 | Marcal | Marca | Mar ValThrargproTrpLysHisValAspAlaIleLysGluAlaLeu 580 MetArgalaLeuGluAsnGluLysAsnGluAspValAspIleIle 600 rleginargprothrcysvalginthrargleulysleufyrlys 620 AsnLeuthrlysLeubsnGlyalaLeuthrmet.lealaSerHis 640 BroprothrProGluthrAspcysGlulleGluvalthrThrPhe 660 AspProSerProLeuGlnArgTyrSerGluAspProThrValPro 420 AlaThrLeuGluArgAlaLysThrLeuSerProGlyLysAsnGly 480 380 440 AsnleuLysGlyPheLeuPheAspIleProPheAspCysTrpLys 680 400 960 360 

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AAD21567
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-MODBL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USFTO spool/US09821883/runat_09092004_105126_6623/app_query.fasta_1.3100
-Q=/cgn2_1/USFTO spool/US09821883/runat_09092004_ININATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UMITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=biuman40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=Epct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-USFR=US09821883 @CGALIGN=Epct -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09821883 @CGN 1 1 1646 @runat_09092004_105126_6623 -NCPU=6 -ICPU=3
-NO_MAAP -LARGEQUERY 'NEG SCORES=0 -WAIT -DSPEDCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=7
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Aad21566 Human HER
Aad21566 Human HER
Aad21568 Human HER
Aat01588 Her-2/neu
Aar11253 Human HER
Aaz60815 Nucleotid
                                                                                 September 10, 2004, 05:04:16; Search time 686.431 Seconds (without alignments) 4313.608 Million cell updates/sec
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5.1.6
Compugen Ltd.
                                                        nucleic search, using frame_plus_p2n model
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GenCore version (c) 1993 - 2004
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Ygapop 10.0,
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Delop 6.0,
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//tag= a //product= "Human HERS00-rGM-CSF fusion protein construct comprising human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular domain, an Ala linker, an ovalbumin (OVA)-derived immunodominant octapeptide, HER-2 membrane distal intracellular domain,
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Human pol
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HER
ERB
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Abx10730
                Abz35012
Abv94128
Abv84128
Acc50139
Acc50139
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Adc09594
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Abz31071
Abz34969
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ABK83918
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Rattus norvegicus.
Unidentified.
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 and
mature rat GM-CSF sequence
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1200 1260 ValAsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAla 460 AACTACCTTTCTACGGACGTGGGATCCGCTAGCATCATTAATTTCGAGAAGTTGGGCGCT 1020 1021 GGGGGGATGGTCCACCACACGCACCCCACTCATCTACCAGGAGTGGCGGTGGGGACTG 1080 1081 ACACTAGGGCTGGAGCCCTCTGAAGAGGGCCCCCCAGGTCTCCACTGGCACCTCCGAA 1140 960 360 400 420 440 120 420 160 180 540 200 9 220 9 240 720 260 780 280 840 300 900 320 340 380 ProbeuAsnAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeuGln GlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArgIle GCTTACGTGCTCATCGCTCACAACTGAGGCAGGTCCCACTGCAGAGGCTGCGGATT LeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGlnLeu CTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAGCTC TGCTACCAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACAACCAGCTGGCTCTC ThrLeuIleAspThrAsnArgSerArgAlaCygHisProCysSerProMetCysLysGly GlylleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGluSer Met ProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysBroTyr AsnTyrLeuSerThrAspValGlySerAlaSerIleIleAsnPheGluLysLeuGlyAla GlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGln LeuProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyr ValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGlyAsp GTGCGAGGCACCCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGCTAGACAATGGAGAC CCGCTGAACAATACCACCCCTGTCACAGGGGCCTCCCCAGGAGGCCTGCGGGAGCTGCAG CysTyrGlnAspThr1leLeuTrpLysAsp1lePheHisLysAsnAsnGlnLeuAlaLeu Acacidatadacaccaaccecircicedecideccaccciditrorcceaignataadecc SerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCysAla GlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCysAla AlaglyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHisSer Gecarcreteaecrecacceaeccreercaccracaacacadacacarreagrec GlyGlyMetValHisHisArgHisArgSerSerTerThrArgSerGlyGlyGlyGlyAspLeu ThrieuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGlu SerLeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValPro crecertergagaergaregeracerrecececergaeergegeeeeegeergaarar 961 1201 421 1321 301 601 321 121 361 141 161 481 181 541 261 281 841 301 901 341 361 381 441 101 421 201 199 241 721 781 401 1261 221

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-MODEL=frame+ p2n.model.-DEV=xlh
-Q=/Cgn2_1/USPTO_gpool/USO9921883/runat_09092004_105127_6631/app_query.fasta_1.3100
-Q=/Cgn2_1/USPTO_gpool/USO9921883/runat_09092004_105127_6631/app_query.fasta_1.3100
-Q=/Cgn2_1/USPTO_gpool/USO9921883/runat_09092004_105127_6631/app_query.fasta_1.3100
-UNITS=b1te -GTART=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi -LIST=45
-UNITS=b1te -GTART=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi -LIST=45
-OUTPWT=ptc -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXLEN=2000000000
-USER=US09921883_@CGN 1 1 16795_@runat_09092004_105127_6631 -NCPU=6 -ICPU=3
-NO MAAAP -LIARGEQUERS -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-FGAPOP=10 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPORT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                    September 10, 2004, 05:41:11; Search time 7467.3 Seconds (without alignments) 4045.651 Million cell updates/sec
                                                                                          US-09-821-883-4
3783
1 MRAAPLLLARAASLSLGFLF........CWKPVQKGAPPPPAHHHHH 697
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                  nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                     3470272 segs, 21671516995 residues
                                                                                                                                                                                                                                                                         Listing first 45 summaries
                                                                                                                             BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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AX129487 Mus muscu
AY116182 Rattus no
BD267515 HER-2/neu
121129 Sequence 14
IS9750 Sequence 14
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AR160259 Sequence

AR167390 Sequence

AR32208 Sequence

X03363 Human c-erb

AR409602 Sequence

AX60703 Sequence

AX66704 Sequence

AX66704 Sequence

BD224136 Novel met

AR41479 Sequence

BD224136 Novel met

AX31479 Sequence

AX31479 Sequence

AX31479 Sequence

AX31479 Sequence

AX3167514 HER-2/neu

AX201817 Sequence

AX316754 Sequence

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AX771418 Sequence
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                                                                                                                                                                                        SUMMARIES
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ARA6060703
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AX467229
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AX644071
AX771418
BD005474
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AR167390
AR392088
HSERB2R
       em_htg_hum: *
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Match Length
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T. T. CAMPATA

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RESULT 1
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3783
1 MRAAPLLLARAASLSLGFLF......CWKPVQKGAPPPPAHHHHHH 697
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMÁRIES

	17	Orv	en	ոյո	ոլո	սյո	eu	en	nio	a]]	us	ոյո	սյո	ոյո	orv	æ
_	B fam	Q8k3f9 rattus norv	Bapi	Q80y89 mus musculi	Q8c0e7 mus musculu	musc	Bapi	Bapi	chyda	lus g	tolag	musc	Q9wvf5 mus musculu	Q9ep98 mus musculu	Q9qx70 rattus norv	sus scrofa
ption	cani	9 rat	homod	enm 6	7 mue	1 mus	homo	homod	9 bra	6 gal	oryc	6 mus	5 mus	8 mu	0 rat	Bua
Description	018735 canis famil	<b>08k3f</b>	29uk79 homo sapien	Q80y8	Q8c0e	Q8r2x	214256	28wyv0	07sy1	Q90836 gallus gall	99bq6¢	09erv	Q9wv£	Q9ep9	099x7	28mi18
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DI DI	01873	08K3	Q9UK79	Q80Y8	0800	Q8R23	01425	Q8WYV(	Q78Y	0908	09BG6	Q9ER	09WV	Q9EP	.x060	<b>DBMIL</b>
	9	7	4	11	11	11	4	4	13	13	9	11	11	11	7	9
ouery Match Length DB	1259	1259	419	711	881	367	165	412	431	527	149	643	655	1210	1209	1209
Query Match	56.5	51.9	42.6	36.5	26.8	25.5	23.9	23.6	22.7	19.9	19.1	19.0	19.0	19.0	18.9	18.7
Score	2136	1962.5	1612.5	1380	1014	996	906	894.5	859	751	723	717.5	717.5	717.5	713.5	708.5
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Q7szf7 brachydanio Q9ese0 rattus norv Q9bud7 homo sapien		Q8vn40 sigmodon hi Q8mlwo drosophila Q9bihy anopheles g Q86nz2 drosophila Q8cfb5 meriones un	Q9myk4 oviв aries Q8wn17 eguus cabal Q95110 eguus cabal Q99144 macaca mula	Q7yrf7 felis silve Q865y5 papio anubi Q9w6f6 gallus gall Q9bq6s oryctolagus	Q23821 caenorhabd1 Q26569 schistosoma Q26566 schistosoma Q26567 schistosoma	Q26568 schistosoma Q9y1x8 ephydatia f Q99j91 marmota mon Q86md7 echinococcu
Q7SZF7 Q9ESE0 Q9BUD7	Q9YH40 Q8AW81 Q9PSH2 P79754	QBVH40 QBMLW0 Q9BIH9 QB6NZ2 QBCFB5	Q9MYK4 Q8WN17 Q95L10 Q9GL44	Q7YRF7 Q865Y5 Q9W6F6 Q9BG64	Q23821 Q26569 Q26566 Q26567	Q26568 Q9Y1X8 Q99J91 Q86MD7
11	555	112221	9999	9 9 13	ດດດດດ	5 11 5
1191 478 331	1165 1305 599 1328	141 1377 1433 1322 145	144 1152 1454 145	141 144 1137 150	1368 366 1717 334	342 1193 138 1564
18.6 18.5 18.4	4. 4. 9. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	. 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	12.1 11.8 11.4 11.2	10.9	9.0	8.8 6.8 1.8
703 701.5 697	658 635.5 610	559.5 543 540.5 471.5	457 429.5 425	417 411 409.5 400.5	341 341 341	321.5 321.5 308 305
17 18 19	2222	2222 2222 242 242	33 32 32	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	66 64 4 60 60 61	4 4 4 4 54 64 67

#### ALIGNMENTS

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O18735

C16735

C16735

C16735

C16735

C16735

C174N-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-JAN-1998 (TrEMBLrel. 25, Last annotation update)

DT 01-JAN-1998 (TrEMBLrel. 25, Last annotation update)

DT 01-JAN-1998 (TrEMBLrel. 25, Last annotation update)

C1 01-CT-2003 (TrEMBLrel. 25, Last annotation update)

C2 Canis familiaris (Dog).

C3 Canis familiaris (Dog).

C4 Canis familiaris (Dog).

C5 Canis familiaris (Dog).

C6 CANA CANA Metazoa; Chordate; Craniata; Vertebrata; Euteleostomi; C6 CANA CANA Metazoa; Chordate; Canis familiaris (Dog).

C6 CANA CANA Metazoa; Chordate; Canis Canis Canis.

C7 CANA CANA Metazoa; Chordate; Canis C
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STRAIN=BDIX;
Watson P.A., Kim K., Chen K.-S., Gould M.N.;
Watsogen-Dependent Mammary Carcinogenesis in Rats Transgenic for the Neu Proto-Oncogene.";
Watsogene.";
We be proto-Oncogene.";
We be proto-Oncogene.";
Watsogene.";
Watsogene."
                                                                                                                                                                                                                                                                966 PRFRELVAEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVP 1025
                                                                                                                                                                                                                                                                                                                                                                             DGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVR 447
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846 AARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESIPPRRFTHQSDVW 905
                                                                                                       SYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECR
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Bukaryota; Metazoa; Chodata; Craniata; Vertebrata; Buteleostomi;
Ammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Last annotation update)
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GO: GO:0005524; F:ATP binding; IEA.
GO: GO:0005524; F:ATP binding; IEA.
GO: GO:0005509; F:calcium ion binding;
GO: GO:000506; F:calcium ion binding;
GO: GO:0006404; F:protein serine/threon
GO: GO:0007169; F:transferase activity;
GO: GO:0007169; F:transferase activity;
GO: GO:0007169; F:transmembrane recepto
InterPro; IPR000249; EF-hand.
InterPro; IPR000219; Furin-like.
InterPro; IPR000219; Furin-like.
InterPro; IPR000219; Furin-like.
InterPro; IPR000219; Fort Kinase.
InterPro; IPR001245; Tyr_pkinase.
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Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep L domain;
Pfam; PF02757; YLP; 2.
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Prodom; PD000001; Prot_Kinase;
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYRKC; 1.
PROSITE; PS00018; EF_HAND; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Rattus norvegicus (Rat)
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306 TDVGSCTLVCPLNNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFA 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNN 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                          6 WCRWGLLIALLPSGAAGTQVCTGTDWKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYL 65
                                                                                                                                                                                                                                                                                                                                                                                                         25 WLDRSVLAKELARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYL
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                         47; Indels 722;
                                                                                                                                                                                                                                                                                                  Length 1259;
                           ProDom; PD000001; Prot Kinase; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TyrKc; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00107; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE DOM; 1.

ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.

SEQUENCE 1259 AA; 137989 MW; E37364D49C4ACD46 CRC64;
                                                                                                                                                                                                                                                                                               56.5%; Score 2136; DB 6; 36.9%; Pred. No. 1.3e-152; tive 22; Mismatches 47;
        PR00109; TYRKINASE
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OM protein - protein search, using sw model

September 9, 2004, 12:20:54; Search time 12.7941 Seconds (without alignments) 2836.691 Million cell updates/sec Run on:

US-09-821-883-4 3783 1 MRAAPLLLARAASLSLGFLF......CWKPVQKGAPPPPAHHHHH 697 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P04626 homo sapien	P06494 rattus norv	певост	gallı	33 homo	33 homo	rattı	79	P21860 homo sapien	P48750 rattue norv	Q62799 rattus norv			-	m			P11052 bos taurus	-	caenor	canie	062757 felis silve	_	002466 branchiosto	P70424 mus musculu		P09208 drosophila			Q25410 lymnaea sta		5127	P14616 homo sapien
SUMMARIES	Ω	ERB2 HUMAN	ERB2_RAT	ERB2 MESAU	EGFR CHICK	ERB4 HUMAN	EGFR HUMAN	ERB4 RAT	EGFR_MOUSE	ERB3 HUMAN	CSF2_RAT	ERB3_RAT	XMRK_XIPMA	EGFR_DROME	CSF2_MOUSE	CSF2_SHEEP	CSF2_CEREL	CSF2_HUMAN	CSF2_BOVIN	CSF2_PIG	LT23_CAEEL	CSF2_CANFA	CSF2_FELCA	CSF2_CAVPO	ILPR_BRALA	ERB2_MOUSE	HTK7_HYDAT	INSR_DROME	INSR HUMAN	INSR MOUSE	MIPR_LYMST	IRR_MOUSE	INSR_RAT	IRR_HUMAN
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	Result No.	1	7	m	4		9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

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246.5 238.5 234.5 234.5 204.5 207 168 168 115.5 150
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### ALIGNMENTS

RESULT 1  RESULT 1  AC D0462  AC D0462  DT 13-AU  DT 13-AU  DT 10-OC  DE REBERS  GN HGREP  GN HGREP  GN HGREP  CO MARINE  REPRES  CO BUKARY  CO C
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                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 164870; -.

ROGENEW; HAUK: 13430; ERBEZ.

ROJ GO:0005012; F:Necu/ErbB-2 receptor activity; TAS.

ROJ GO:0004716; F:receptor signaling protein tyrosine kinase ...; TAS.

ROJ GO:0004716; F:receptor signaling protein tyrosine kinase ...; TAS.

ROJ GO:0004716; P:enzyme linked receptor protein signaling pa. ..; TAS.

ROJ GO:000440; P:protein amino acid dephosphorylation; TAS.

ROJ GO:0006470; P:protein amino acid dephosphorylation; TAS.

RICEPTO: IPR0006211; Furin-Tike.

RICEPTO: IPR0006212; Furin-Tike.

RICEPTO: IPR0006212; Furin-Tike.

RICEPTO: IPR0001245; TYL Dikinase.

RICEPTO: IPR000693; Pirinase; 1.

REAM: PR00069; Pirinase; 1.

REAM: PR00109; TYRKINASE.

RODOM: PR00109; TYRKINASE.

RODOM: PR00109; TYRKINASE.

ROSOTTE: PS00107; PROTEIN KINASE ATP; 1.

RESIDER: RS00107; PROTEIN KINASE ATP; 1.

RESIDER: RS00107; PROTEIN KINASE ATP; 1.

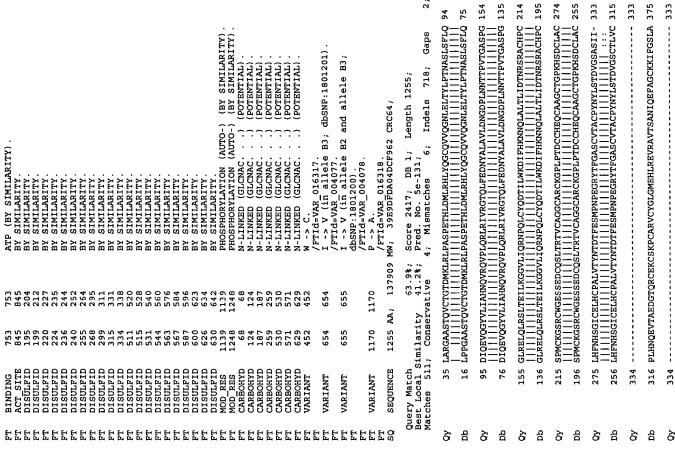
ROSOTTE: PS00101; PROTEIN KINASE DOM; 1.

REPROFERENCE AND SECTION RICEPTOR REPROFEIN RICEPTOR ROMENTAL.

REPROFERENCE AND SECTION RICEPTOR R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAS.
                                                                                                  residues (By similarity).

POLYMORPHISM: There are fours alleles due to the variations in politions 654 and 655. Allele BI (Ile-654/N16-655) has a frequency of 0.782; allele B2 (Ile-654/Val-655) has a frequency of 0.182; allele B3 (Val-654/Val-655) has a frequency of 0.012.

SIMILARITY: Belongs to the EGF receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
 alpha and amphiregulin.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                            tyrosine phosphate.
SUBUNIT: Heterodimer with each of the other ERBB receptors SUBCHILULAR I.OCATION: Type I membrane protein.
PTM: Ligand-binding increases phosphorylation on tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                            EMBL, M11767; AAA35808.1; --
EMBL, M11761; AAA35808.1; JOINED.
EMBL, M11761; AAA35808.1; JOINED.
EMBL, M11764; AAA35808.1; JOINED.
EMBL, M11764; AAA35808.1; JOINED.
EMBL, M11765; AAA35808.1; JOINED.
EMBL, M11765; AAA35808.1; JOINED.
EMBL, M1730; AAA75493.1; --
EMBL, M2036; AAA35978.1; --
EMBL, AY208911; AAO18082.1; --
EMBL, XO3363; CAA27060.1; --
PDB; 1N82; 18-FEB-03.
PDB; 1N82; 18-FEB-03.
PDB; 10R1; 01-JAN-00.
GGnew, CANNO.3430; ERBB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1255
652
675
1255
987
734
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TRANSMEM
DOMAIN
DOMAIN
NP_BIND
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- protein search, using sw model OM protein 9, 2004, 12:29:10 ; Search time 22.2506 Seconds (without alignments) 3013.200 Million cell updates/sec September Run on:

score: Title: Perfect sc Sequence:

US-09-821-883-4 3783 1 MRAAPLLLARAASLSLGFLF.......CWKPVQKGAPPPAHHHHH 697

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Length	98	ID	Description
	2417	63.9		-	A24571	protein-tyrosine k
7	1962	51.9	1260	-	TVRTNU	protein-tyrosine k
m	1946.5	51.5	-	~	148161	p-185 precursor -
4	752	19.9	_	-	TVCHLV	epidermal growth f
S	751	19.9		~	A42032	
ø	723.5	19.1	1308	~	A47253	
7	719.5	19.0	1210	Н	GOHUE	
æ		19.0	_	~	A53183	
σ	713.5	18.9		N	A36325	
10	697	18.4	1342	~	A36223	Н
11	683	18.1		~	146269	granulocyte-macrop
12	662	17.5		7	JC4387	epidermal growth f
13	651	17.2	1166	-	806142	protein-tyrosine k
14	539.5	14.3	843	7	A27131	epidermal growth f
15	473	12.5	153	Н	FOMSGM	granulocyte-macrop
16	461	12.2	144	7	JH0469	granulocyte-macrop
17	457	12.1	144	Н	A61632	granulocyte-macrop
18	442	11.7	144	-	FOHUGM	granulocyte-macrop
19	421.5	11.1	143	-	FQBOGM	granulocyte-macrop
50	404.5	10.7	1323	7	E88257	protein let-23 (im
21	404.5	10.7	1374	N	870712	protein-tyrosine k
22	396.5	10.5	144	~	A44936	granulocyte-macrop
23	390.5	10.3	1369	~	870713	protein-tyrosine k
24	379	10.0	-	Н	GOFFE	epidermal growth f
25	341	9.0		~	D45558	
26	341	9.0	1717	Н	A45558	
27	331	8.7	333	N	B45558	epidermal growth f
28	331	8.7	342	~	C45558	epidermal growth f
29	318	8.4	1363	~	T43220	insulin-like growt

protein-tyrosine k insulin receptor ( insulin receptor -		insulin receptor p insulin receptor-r	insulin-like growt insulin-like growt	tyrogine Kinage re ingulin receptor-r ingulin receptor-r	insulin-like growt insulin receptor -	insulin receptor h
T18534 S57245 A56081	INHUR A34157 T43212	A36080 A36502	IGHUR1 A33837	JH0803 B47417 B36502	A48805 T30346	T42047
777	H 62 62	0 0	п 70 г	0 0 0	0 0	7
1477 2101 2148	1382 1372 1607	1383	1367	183 540 1268	329 1390	1846
7.3	6.9	6.6	6.00	9 9 9	0.0	5.0
276.5 271 271	258 252.5 252	249 246.5	238.5	235.5 233.5 231.5	224.5	188
30 31	33 34 35	36 37	398	4 4 4 0 1 2	44	45

#### ALIGNMENTS

```
Diocein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB (;Species Homo sapiens (man) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Accession: A24571
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A; Molecule type: mRNA
A; Residues: 1-1255 < YAM->
A; Residues: 1-1255 < YAM->
A; Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
A; Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
B; Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
Broc. Natl. Acad. Sci. U. S.A. 63. 6497-6501, 1985
A; Title: A V-erbB related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epiderm A; Reference number: A25491; MUID:86016729; PMID:2995967

A,Molecule type: DNA A,Residues: 73-1031 <SEM> A,Gross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282 A,Gross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282 R,Goussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P S,Gance 230, 1132-1139, 1985 A,Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromos A,Reference number: A44188; MUID:86070181; PMID:2999974

A; Accession: A44188

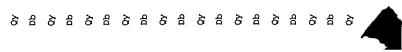
A;Molecule type: DNA A;Residues: 740-910 <COU1> A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A;Accession: B44188

A; Molecule type: mRNA A; Residues: 1.517, RALL, 522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2> A; Cross-references: GB:M11730; NID:g183986 A; King, C.R.; Kraus, M.H.; Aaronson, S.A. Science 229, 974-976, 1985 A; Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma. A; Reference number: 159509; MUID:8572597; PMID:2992089

A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: GB:L22395; NID:g459807; PIDN:AAA35809.1; PID:g459808
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional
A;Reference number: I57622; MUID:87286898; PMID:3039351

A,Accession: I57622 A,Status: translated from GB/EMBL/DDBJ Monlecule type: DNA A,Residues: 1-191 <TAL>

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C; Genet		Qy 334	333
A;Gene: A;Cross	GDB:ERBB2; NGL; NEU; HER-2 rreferences: GDB:120613; OMIM:164870	Db 676 KRRQQKIRKYTWRRLLQETELVEPLTPSG	KRRQQKIRKYTWRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 735
A, Map p	osition: 1/q21.1-1/q21.1 ns: 25/1; 75/3; 147/1; 883/3	Qy 334	333
A; Note: C; Funct.		Db 736 KGIWIPDGENVKIPVAIKVLRENTSPKAN	KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ 795
A; Descr C; Super	rosine residue se homology	Qy 334	333
c; keywo inase	ras: Alr; aucopnospnorylation; auplication; glycoprotein; phospho	Db 796 LVTQLMPYGCLLDHVRENRGRLGSQDLLN	LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS 855
F; 1-21/	Domain: signal sequence #status predicted <21G> 55/Product: protein-tyrosine kinase erbs2 #status predicted <mat></mat>	Ογ 334	333
F; 22-65	4	Db 856 PNHVKITDFGLARLLDIDETEYHADGGKV	PNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESILRRRFTHQSDVWSYGVTVWEL 915
F,395-6	05/Domain: EGF receptor extracellular domain repeat <ee2> 75/Domain: transmembrane #status predicted <tmm></tmm></ee2>	Qy 334	338
F;718-9	255/Domain: intracellular #Status predicted <1N1> 33/Domain: protein kinase homology KINN> (Comming Protein thinse homology KINN)	Db 916 MTFGAKPYDGIPAREIPDLLEKGERLPQF	MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE 975
F; /26-/ F; 68, 12	F;726-734/Region: procein Ainase Air-Dinding Mouli F;68,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predict D:68/Dinding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted	Qy 339	338
F;753/A	(by autophosp	Db 976 FSRMARDPQRFVVIQNEDLGPASPLDSTF	
Query Best 1	1255;	Qy 339GAGGWVHHRHRSSSTRSGGGDLTLGLE	CACGMVHRHRSSSTRSGGGDLTLGLEPSEEAPRSFLAPSEGAGSDVPDGDLGWGAA 396 
Match	vative 4; Mismatch	TSS4TAALASTODESTODESTABLESET	DGYVAPLICSPOPEYVNOPDVRPOPPSPREG 456
۶۵ ور د	35 LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ 94	1096	
} &	DIOEVOGYVLIAHNOVROVPLORRIVRGTOLFEDNYALAVLDNGDPLNNTTPVTGASPG 1	Qy 457 PLPAARPAGATLERAKTLSPGKNGVVKDV ON 1164 DLPAARPAGATLERPAKTLSPGKNGVVKDV ON 1164 DLPAAPPAGATLEPPKTLSPGKNGVKDV	PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENDEYLTPGGGAAPQPHPPPAFSP 516
qq	76 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 135	517	555
S Q	155 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC 214		
δ	215 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC 274	ESULT 2	
qa	196 SPMCKGSRCWGESSEDCQSLTRIVCAGGCARCKGPLPTDCCHEQCAAGCTGFKHSDCLAC 255	rotein-tyrosine kinase (EC 2.7.1.112) neu :Species: Rattus norvegicus (Norway rat)	precursor - rat
දු දු	275 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSASII- 333	C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999 C;Accession: A24562; A61204 R;Bargmann, C:I:; Hung, M.C.; Weinberg, R.A.	<pre>bec-1988 #text_change 11-Jun-1999 1.</pre>
ò	334 333	lature 319, 226-230, 1986 Title: The neu oncogene encodes an epider	mal growth factor receptor-related protein.
g G	316 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 375	JRELEIEINCE HUMBEL: AZ*30Z; MOID:0011000Z; JACCESSION: AZ\$50Z :MOIECUIE TVDE: MRNA	11704000
ò	334 333	Residues: 1-1260 <bar> Cross-references: EMBL:X03362: NID:956745</bar>	; PIDN:CAA27059.1; PID:956746
qa	376 FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI 435	() Masui, T.; Mann, A.M.; Macatee, T.L.; Gar arcingenesis 12, 1975-1978, 1991	land, E.M.; Okamura, T.; Smith, R.A.; Cohen,
ò	334 333	Vilities Direct DNA sequencing of the rat nethiazolv11 formamide or N-methy1-N-nitrosc	<pre>leu oncogene transmembrane domain reveals no mi urea.</pre>
qq	436 LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 495	I,Reference number: A61204; MUID:92035293; ACCESSION: A61204	PMID:1682063
ઠે	334 333	Status: preliminary	
qa	496 TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV 555	(), Residues: 677-663, VV, 665-702 < MAS> (NOTE: authors translated the codon GCA fo	or residue 25 as Val
ò	334 333	C,Genetics: A:Gene: neu	
qa	556 NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615	Superfamily: epidermal growth factor rece :/Superfamily: epidermal growth factor rece :/Keywords: ATP: autophosphorylation: dubli	ptor; protein kinase homology cation; glycoprotein; phospho
ò	334 333	;1-19/Domain: signal sequence #status prec;;20-1260/Product: protein-tyrosine kinase	F:1-19/Domain: signal sequence #status predicted <sig> F:20-1260/Product: protein-tyrosine kinase neu #status predicted <mat></mat></sig>



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September 9, 2004, 12:41:37; Search time 73.7051 Seconds (without alignments) 3032.635 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                     3783
1 MRAAPLLLARAASLSLGFLF.......CWKPVQKGAPPPPAHHHHH 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence	Sequence	Sequence	Sequence	Sequence										
SUMMARIES	US-09-821-883-4	US-09-821-883-2	US-09-821-883-3	US-09-821-883-1	US-09-854-356-6	US-09-821-883-5	US-09-811-123-9	US-09-811-115-3	US-09-769-508-2	US-09-984-092-4	US-10-177-293-126	US-10-207-498-6	US-10-338-730-2	US-10-322-892-4	US-10-272-437A-28
80	6	0	σ	σ	σ	σ	σ	თ	σ	12	14	14	14	14	15
% Query Watch Length DB	697	069	564	555	919	479	1255	1255	1255	1255	1255	1255	1255	1255	1255
* Query Match	100.0	91.8	79.7	78.2	68.3	65.5	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0
Score	3783	3473.5	3014	2957.5	2585	2478	2422	2422	2422	2422	2422	2422	2422	2422	2422
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Sequence 594, App	Sequence 36, Appl	Seguence 4, Appli	Sequence 126, App	н	Sequence 2, Appli	Sequence 6, Appli				Sequence 3, Appli	4	'n	H	Sequence 553, App	Sequence 4641, Ap	Sequence 68, Appl	Sequence 4641, Ap	Seguence 72, Appl	Sequence 14, Appl	Sequence 118, App	Sequence 118, App	Sequence 2, Appli	Sequence 1, Appli	-	Sequence 13, Appl	Sequence 3, Appli	Sequence 4, Appli	Sequence 11, Appl	Sequence 7, Appli
US-10-117-937-594	US-10-435-696-36	US-10-441-779C-4	US-10-734-564-126	US-09-854-356-1	US-09-930-125-2	US-09-441-411-6	US-10-469-162-3	US-10-253-286-553	US-09-765-973-2	US-10-418-027-3	US-10-207-655-45	US-10-313-644-2	US-10-394-322A-17					US-10-146-473-72	US-09-854-356-14	US-09-870-759-118	US-09-751-708A-118	US-09-854-356-2	US-09-921-161-1	US-10-268-501-13	US-10-608-626-13	US-09-854-356-3	US-10-412-804A-4	US-10-412-804A-11	US-09-854-356-7
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64.0	64.0	64.0	64.0	63.9	63.9	63.9	63.9	63.9	63.9	63.9	63.9	63.9	63.9	63.9	63.9	63.9	63.9	63.7	52.2	51.9	51.9	51.8	42.7	42.7	42.7	42.7	42.7	42.7	42.7
2422	2422	2422	2422	2417	2417	2417	2417	2417	2417	2417	2417	2417	2417	2417	2417	2417	2417	2410	1974.5	1962	1962	1959.5	1614.5	1614.5	1614.5	1614.5	1614.5	1614.5	1614.5
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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61 HLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 3783; DB 9; Length 697; Best Local Similarity 100.0%; Pred. No. 2e-258; Matches 697; Conservative 0; Mismatches 0; Indels 0;
                                                                         APPLICANT: Laus, Reiner
APPLICANT: Laus, Reiner
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Call-Based Immunotherapy
TITLE REPERBERS: 736-0022.30
CURRENT APPLICATION NUMBER: US 60/193,504
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR APPLICATION NUMBER: US 60/193,504
NUMBER OF SEQ ID NOS: 30
SOFTWARR: FRAEESEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: HER500*-rGM-CSF construct
; Sequence 4, Application US/09821883; Patent No. US20020061310A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORM
US-09-821-883-4
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541 TPTAENPEYLGLDVPAAAPTRSPNPVTRPWKHVDAIKEALSLLNDMRALENEKNEDVDII 600
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Sequence 3, Application US/09821883;
Patent No. US20020061310A1
GENERAL INFORMATION:
APPLICANT: Laus, Reiner
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Coll-Based Immunotherapy
FILE REFERENCE: 756-0022.30
CURRENT FILLING DATE: 2001-03-30
CURRENT FILLING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENTING IN SEC. Windows Version 4.0
SEQ ID NO 3
LENTING THE SEQ ID NOS: 30
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100.0%; Pred. No. 3e-204;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: HERSOO* construct US-09-821-883-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 79.7%; 'Best Local Similarity 100.0%; Matches 558; Conservative 0
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                                                                                                                   GGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFES 300
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CYQDTILWKDI FHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA
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91.8%; Score 3473.5; DB 9; Length 690;
Best Local Similarity 91.7%; Pred. No. 1.4e-236;
Matches 641; Conservative 19; Mismatches 28; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09821883

Patent No. US20020061310A1

GENERAL INFORMATION:

APPLICANT: Laus, Reiner

APPLICANT: Laus, Reiner

TITE OF INVENTION: Compositions and Methods for Dendritic

TITE OF INVENTION: Compositions and Methods for Dendritic

TITE OF INVENTION: Cell-Based Immunotherapy

FILE REFERENCE: 7636-0022.30

CURRENT APPLICATION NUMBER: US/09/821,883

CURRENT APPLICATION NUMBER: US 60/193,504

PRIOR PILING DATE: 2000-03-30

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 690
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US-09-821-883-2
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US-09-821-883-2
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5; Search time 20.3037 Seconds (without alignments) 1772.256 Million cell updates/sec
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-821-883-4 Title: Perfect score: Sequence:

Scoring table:

389414 segs, 51625971 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
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/cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Issued Patents AA:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appli	Appli	Appl	Appl	Appl	Appli	Appl	Appli	Appl	Appl	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appl	Appl	App1	Appl	Appl	Appli	Appl	Appli	Appli	Appli
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Description		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ID	US-09-527-487-2		US-08-467-083-68	US-08-414-417B-68	-486	US-08-625-101-2	-08-	US-08-356-786-2	US-08-466-680B-68	US-09-354-533-68	08-484-	US-09-146-283-4	US-08-579-823A-4	US-09-344-195-4	US-09-630-155-2	US-08-422-108-1	US-08-422-734-1	US-08-414-417B-69	-08-486-348A-6	US-08-468-545B-69	US-08-466-680B-69	US-09-354-533-69	US-09-648-067A-1	US-08-484-438-10	US-08-484-438-4	US-08-484-438-2	US-08-336-708A-9
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#### ALIGNMENTS

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95 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 154
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5; Indels 718;
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Pred. No. 2.2e-187;
4; Mismatches 5; Indels 718
           Sequence 2, Application US/09527487
Patent No. 6528060
GENERAL INFORMATION:
APPLICANT: NICOLEUCE, Charles
TILLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
FILE REFERENCE: 12688130920
CURRENT APPLICATION NUMBER: US/09/527,487
CURRENT FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
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41.3%;
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Best Local Similarity 41.3
Matches 512; Conservative
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CORGANISM: Homo sapiens
US-09-527-487-2
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US-09-527-487-2
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                                                                            Score 2422; DB 4;
Pred. No. 2.2e-187
4; Mismatches 5
                                                                            Query Match
Best Local Similarity 41.3%;
Matches 512; Conservative
SEQ ID NO 3
LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
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                           436 LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 495
                                                                               496 TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV 555
                                                                                                                                  556 NARHCLPCHPECQPQNGSVTCFGPBADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615
                                                                                                                                                                                      616 FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILI 675
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Patent No. 6632379;
GENERAL INFORMATION:
APPLICANT: Erickeon, Sharon
APPLICANT: Schwall, Ralph;
APPLICANT: King, Kathleen
TILE OF INVENTION: HER-2 TRANSCENIC NON-HUMAN TUMOR MODEL;
FILE REFERENCE: GENENT.034A;
CURRENT APPLICATION NUMBER: US/09/811,115
CURRENT FILING DATE: 2001-03-16;
PRIOR APPLICATION NUMBER: 60/189,844
PRIOR PILICATION NUMBER: 60/189,844
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-811-115-3
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916 MTFGAKPYDGI?AREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE 975

PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 915

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9, 2004, 12:20:15; Search time 76.7646 Seconds (without alignments) 2565.449 Million cell updates/sec
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1 MRAAPLLLARAASLSLGFLF.......CWKPVQKGAPPPPAHHHHH 697
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Compugen Ltd.
GenCore version
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Perfect score:
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1586107 Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues BLOSUM62 . Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Sequence:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\*
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geneseqp2001s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* A\_Geneseq\_29Jan04:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Aae13111 Human HER	Aae13109 Human HER	Aae13110 Human HER	8 Human	Human	8 Her-2/	Aael3112 Human HER	Aay92620 Human her	Aab60167 HER2 tran	Aae12130 Human tyr		Aae26366 Human Her	Aau74545 Human HER	Abr47447 Breast ca	Abp74708 Human Her	Aae38390 Human c-e	Ada38143 Human erb	Ada37255 Human Erb	Adb67621 Human epi	Aar39568 Sequence	Aaw01111 HER-2/neu	Aaw92406 Human HER	Aay84780 Amino aci	Aab21198 Human HER	Aag88267 HER2/neu
	ID	AAE13111	AAE13109	AAE13110	AAE13108	AAB21203	AAM51148	AAE13112	AAY92620	AAB60167	AAE12130	AAE26349	AAE26366	AAU74545	ABR47447	ABP74708	AAE38390	ADA38143	ADA37255	ADB67621	AAR39568	AAW01111	AAW92406	AAY84780	AAB21198	AAG88267
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Aab85458 Human HER	Aae20479 Human Her	Aau77114 Human Her	_	Aae24067 Human Her	Abr43687 Human c-e	Abr82066 Human Her	Adc09593 Her2/Neu	Add25484 Binding d		_	Adc35106 Human bre	~	Aam51152 Mouse Her	Aam51153 Mouse Her	Aab21208 Human HER	Aaw19764 Her2-GM-C	Aab21206 Mouse Her		Aam51151 Mouse Her
AAB85458	AAE20479	AAU77114	AAM51143	AAE24067	ABR43687	ABR82066	ADC09593	ADD25484	ADE63281	ADE76190	ADC35106	AAU98923	AAM51152	AAM51153	AAB21208	AAW19764	AAB21206	AAG62860	AAM51151
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#### ALIGNMENTS

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Immunostimulatory fusion protein, IPP, antigen component, therapy, immunostimulatory component, T-cell mediated immune response, DC, dendtitic cell; colon cancer, breast carcinoma; ovarian cancer, PAP protein, Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; GM-CSF; HER-2 protein; granulocyte-macrophage colony stimulating factor; ovalbumin-derived octapeptide; OVA; rat; HER500-rGM-CSF fusion protein.
                                                                                                                                                                                                                                                                           Human HER500-rGM-CSF fusion construct comprising OVA-derived peptide.
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                             AAE13111 standard; protein; 697
                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                28-JAN-2002
                                                                                                                AAE13111;
AAE1311
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Graddis T; 30-MAR-2000; 2000US-0193504P. 30-MAR-2001; 2001WO-US010515. (DEND-) DENDREON CORP Vidovic D, Rattus norvegicus. Unidentified. WO200174855-A2. Homo sapiens. 11-OCT-2001. Chimeric. Laus R, 

An immunostimulatory fusion protein comprising the intracellular domain of HER-2 and an antigen elicits an immune response to the antigen and is useful for the treatment of associated cancer associated. N-PSDB; AAD21567.

WPI; 2001-662965/76.

Claim 7; Page 27; 59pp; English.

The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to

(first entry)

28-JAN-2002

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immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HERSOO rGM-CSF fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular domain, an Ala linker, an ovalbumin (OVA)-derived immunodominant octapeptide, HER-2 membrane distal intracellular domain, an Ala linker, a mature rat granulocyte-macrophage colony stimulating factor (GM-CSF) sequence and a C-terminal tag
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protective dendritic cell (DC) -induced T-cell mediated cellular
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AAE13109 standard; protein; 690

RESULT 2 AAE13109 AAE13109,

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The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intraccellular domain of HBR-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HBR500 hGM-CSF fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HBR-2 signal sequence, mature HBR-2 membrane distal extracellular and intracellular domains, an Ala Ala linker amature human granulocyte- macrophage colony stimulating factor (GM-CSF) sequence and a C-terminal tag
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                                                       Immunostimulatory fusion protein; IFP; antigen component; therapy; immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; pAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; GM-CSF; HERR-2 protein; granulocyte-macrophage colony stimulating factor; HERSOO-hGM-CSF fusion protein.
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91.7%; Pred. No. 2.3e-222;
ive 19; Mismatches 28; Indels 11;
                              Human HER500-hGM-CSF fusion protein construct.
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Perfect score: Sequence:

US-09-821-883-3 3062 1 MRAAPLLLARAASLSLGFLF.......ENPEYLGLDVPAAAHHHHH 564

**BLOSUM62** Scoring table:

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27513289 seqs, 14931090276 residues Searched: 55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Command line parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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-Q=/Cgn2\_1/USPTO\_spool/USO9821883/runat\_09092004\_105127\_6643/app\_query.fasta\_1.3100
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-DOOPEXT=2 - START=1 - MINNATGH=0.1 -LOOPCL=0 -LOOPEXT=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USFR=US09821883\_GCGN\_1 1.1571\_Grunat\_09092004\_105127\_6643 -NCPU=6 -ICPU=3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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#### ALIGNMENTS

RESULT 1 AK031099 LOCUS DEFINITION

AAUJ1099
Mus musculus 13 days embryo forelimb CDNA, RIKEN full-length enriched library, clone:5930404N10 product:v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived AKO31099

AK031099.1 GI:26082143 HTC; CAP trapper. Mus musculus (house mouse) Mus musculus YERSION KEYWORDS SOURCE ORGANISM ACCESSION

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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AUTHORS

TITLE

REFERENCE

JOURNAL MEDLINE

TITLE

AUTHORS

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xref="FANTOM DB:5930404N10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adachi, J. Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashida, K., Hayashida, K., Hayashida, K., Hayashida, K., Hayashida, K., Hirozane, T., Haramto, K., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyan, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, A., Murata, M., Santo, R., Saltoh, H., Sakai, C., Sakai, K., Sakai, K., Saltoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Takada, Y., Tanaka, T., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                     Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4323)
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Encyclopedia Project of Genome Exploration Research Group in Riken
  dammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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                                             Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/organism="Mus musculus" /mol\_type="mRNA" /strain="C57BL/6J"

FEATURES

COMMENT

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v-erb-b2 erythroblastic leukemia viral oncogene homolog 2,
neuro/glioblastoma derived oncogene homolog (avian)
(MGD|MGI:95410, GB|U71126, evidence: BLASTN, 99%,
                                                          enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeuGluLeuThr
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Mismatches:
Indels:
Gaps:
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September 10, 2004, 15:10:16

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Run on:

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Searched:

**BLOSUM62** 

Scoring table:

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Sequence 7, Appl
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Sequence 10, Appl
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Sequence 7, Appli
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Sequence 11, A
Sequence 125,
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Sequence 595,
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Sequence 5,
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APPLICANT: Laus, Reiner
APPLICANT: Offactor Damir
APPLICANT: Graddis, Thomas
TITLE ON INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REPERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
SPRIOR FILING DATE: 2000-03-30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 30
THOMAS OF THE OFF US-09-821-883-8
US-09-821-883-9
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US-09-821-883-9
US-09-821-883-6
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OTHER INFORMATION: HER500* construct
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1 MRAAPLLLARAASLSLGFLF......BNPEYLGLDVPAAAHHHHH
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      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

SUMMARIES

Query Match Length DB

Score

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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09821883;
Sequence 9, Application US/09821883;
Patent No. US20020061310A1
GENERAL INFORMATION:
APPLICANT: Laus.
TITLE OF INVENTION: Compositions and Methods for Dendritic;
TITLE OF INVENTION: Compositions and Methods for Dendritic;
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT FILING DATE: 2001-03.30
FRIOR APPLICATION NUMBER: US 60/193,504
FRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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1681 CATCACCATCAC 1692
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Title: Perfect score:

Sequence:

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Scoring table:

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US-08-229-515A-9

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2 Sequence 9, Application US/08229515A

3 Sequence 9, Application US/08229515A

3 Patent No. 5518885

3 APPLICANT: RAZIUDDIN

4 APPLICANT: RAZIUDDIN

APPLICANT: SARKAR, FAZLUL H

APPLICANT: SARKAR, FAZLUL H

APPLICANT: SARKAR, FAZLUL H

TITLE OF INVENTION: NEOPLASTIC DISEASE

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: NEEDLE & ROSENBERG PC

STREET: 127 Peachtree Street, Suite 1200

CITY: Atlanta

STATE: Georgia

COUNTRY: usa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIFICATION: 435
1414.608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFRENCE/DOCKET NUMBER: 1414,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 4530 base pairs
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     Command line parameters:
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-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09821883/runat_09092004_105128_6657/app_query.fasta_1.3100
-Q=/cgn2_1/USPTO_spool/US099821883/runat_09092004_MINATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=b1ts -START=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE==pct -THR_MAX=100 -THR_MINEN=0 -ALIGN=15.
-MODEL-CAL.-OUTFMT=pco -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09821883_@CGN 1 1 215_@runat_09922004_105128_6657 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPEDACK==100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=300 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=7
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1 mraaplillaraasisigfif.......sendeylgidupaahhhhh 564
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/cgn2 e/ptodata/2/ina/5A COMB.seq:*
/cgn2 e/ptodata/2/ina/5B COMB.seq:*
/cgn2 e/ptodata/2/ina/6A_COMB.seq:*
/cgn2 e/ptodata/2/ina/6A_COMB.seq:*
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/cgn2 e/ptodata/2/ina/PCTUS COMB.seq:*
/cgn2 e/ptodata/2/ina/PCTUS COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                      - nucleic search, using frame plus p2n model
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US-08-645-865-9
US-09-167-322-4
US-09-877-17A-11
US-09-817-17A-11
US-09-817-115-1
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US-09-663-834A-3
US-09-663-814A-3
US-08-652-101-1
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Listing first 45 summaries
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Database :

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                                                                                                  ArgalaalaaroLeuLeuLeuAlaargala-----AlaSerLeuSerLeuGly 17
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                        1.86e-189
2427.50
41.61%
40.91%
79.28%
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-229-515A-9
                                              Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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à	298	PheGluSerMet ProAsnProGluGlyArgTyrThrPheGlyAlaSerCy8ValThrAla 317
qa	985	TTTGAGTCCATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCCAGCTGTGTGACTGCC 1044
λ	318 (	CysproTyrAsnTyrLeuSerThrAspValGlySerAlaSerIleIle 333
qo	1045	
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qa	1105	AACCAAGAGGTGACAGAGGATGGAACACAGGGGTGTGAGAAGTGCAGCAAGCCCTGT 1164
οy	333	333
q	1165 (	GCCCGAGTGTGTGTTATGGTCTGGGGCATGGAGCACTTGCGAGAGGTGAGGGCAGTTACCAGT 1224
λά	333	333
අ	1225 (	GCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCG 1284
à	333	333
q	1285 (	GAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGGCTCCAGGCAGCAGCTCCAA 1344
λά	333	333
qa	1345 (	GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC 1404
λ'n	333	333
ą	1405 (	CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAAT 1464
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à	333	333
qq	1525	AGGGAACTGGGCAGTGGACTGGCCCTCATCCACATAACACCCCACCTCTGCTTCGTGCAC 1584
à	333	333
q	1585	ACGGIGCCCIGGGACCAGCICTITCGGAACCCGCACCAAGCICTGCTCCACACTGCCAAAC 1644
λα	333	333
q	1645 (	CGGCCAGAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGCCCCGAGGG 1704
λά	333	333
q	1705 (	CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAG 1764
à	333	333
q	1765 (	GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGG 1824
λά	333	333
QD	1825 (	CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCCAGAATGGCTCAGTGACCTGTTTTGGA 1884
λά	333	333
q	1885 (	CCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCT
λά	333	333
q	1945 (	CGCTGCCCCAGCGGTGTGAAACCTGACCTCCTACATGCCCCATCTGGAAGTTTCCAGAT 2004
λά	333	333
QQ Q	2005	GAGGAGGGCGCATGCCATCCCCCATCAACTGCACCCCACTCCTGTGTGGACCTGGAT 2064

Human gen Breast ca Human cDN

Human Her Human c-e

Breast ca

HER-2 tra Human HER

CDNA enco

Human HER-2

Binding d Human epi Human her Human ERB Human ERB Human HER Human Her Human Her Human Her

Abk 83918
Acc50139
Acc50139
Adc09594
Adc19537
Adc19537
Adc35148
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Adx3933
Abx1986
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Abx1986
Abx19333
Adx3333
Adx3333

c-e bre

Human Human

Human

Human

HER2 tran HER-2/neu Human HER Human HER

Human

Human Human

Human CDN

Aaq46083

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Minimum DB Maximum DB

Searched:

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comprising human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular domain, an Ala linker, an ovalbumin (OVA) -derived immunodominant octapeptide, HER-2 membrane distal intracellular domain and a C-terminal tag"
//note= "CDS does not include stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                          Human HER500 fusion DNA construct comprising OVA-derived octapeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunostimulatory fusion protein; IFP; antigen component; therapy; immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; OVA; HER-2 protein; ovalbumin-derived octapeptide; HER500 fusion DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "Human HER500 fusion protein construct
                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                            ABZ34969
AAD38904
ACC69999
ADC35148
                                                                                                                                             ADD25483
ADB67620
AAA09455
ABV78168
ABZ35744
AAD43935
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ABK14058
ABL91709
ACC57649
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AAQ46083
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1. .1692
                                                                                                                                                                                                                                                                                                                                                                        AAD21566 standard; DNA; 1692
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                                                                                           3768
3768
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Homo sapiens.
Unidentified.
Chimeric.
224255
244237.5
244227.5
24427.5
24277.5
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 Aad21567 Human HER
Aad21565 Human HER
Aad21565 Human HER
Aat71253 Human HER
Aaz60815 Nucleotid
Aad19731 Human tyr
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Aad21567 Human HER
Aad21564 Human HER
Aad21565 Human HER
                                                          6 ; Search time 555.448 Seconds (without alignments) 4313.608 Million cell updates/sec
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                                                                                                            ......ENPEYLGLDVPAAHHHHH
        5.1.6
Compugen Ltd.
                                         nucleic search, using frame_plus_p2n model
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                              3373863 segs, 2124099041 residues
         version:
                                                          September 10, 2004, 05:04:16
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        GenCore (c) 1993
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Database :

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Score

Result

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                                             ProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeuGln
                                                        crrcaaagccrcacagagarcrrgaaaggaggggrcrrgarccagggaagggggggcrc
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                      GTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGCTAGACAATGGAGAC
                                                                                                                                        CysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAlaLeu
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ALIGNMENTS

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KEYWORDS		qq	661 rcccccrccrcccccasas
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FEATURES		ογ	281 GlylleCysGluLeuHisCy
	<pre>/organism="synthetic construct" /mol_type="unassigned DNA"</pre>	Ор	841 GGCATCTGTGAGCTGCACTG
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PEDUBNICE FROM N.A.

YOKOLA H.;

YOKOLA H.;

YOKOLA H.;

"CDNA clouding of erbB-2 from canine mammary gland.";

BMBL; AB008451; BAA23127.1; -.

BMBL; AB008451; BAA23127.1; -.

BMBL; AB008451; ErdR.

GO; GO:0005524; F.ATP binding; IEA.

GO; GO:0005509; F.calcium ion binding; IEA.

GO; GO:0005509; F.calcium ion binding; IEA.

GO; GO:0005006; F.epidermal growth factor receptor activity; IEA.

GO; GO:0005006; F.epidermal growth factor receptor activity; IEA.

GO; GO:000506; F.epidermal amino acid phosphorylation; IEA.

GO; GO:000740; F.transmembrane receptor protein tyrosine kin. ..; I

RI CEPPO; IPR00494; EGFR_L domain.

InterPro; IPR00494; EGFR_L domain.

InterPro; IPR004019; Furl Title.

InterPro; IPR004019; Furl Title.

InterPro; IPR004019; YLP motif.

INTERPRO; IPR0069; IRINIANSE; INTERPRO; IRR04010; YLP motif.

INTERPRO; IPR0069; IRR04019; YLP motif.

INTERPRO; IRR04019; YLP motif.

INTERPRO; IRR04019; YLP motif.

INTERPRO; IRR04019; YLP motif.
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Mammalia; Eutheria; Carnivora; Rissipedia; Canidae; Canis.
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Last annotation update)
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PF01030; Recep L domain; 2.
PF02757; YLP; 2.
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Q80Q99 mus musculu
Q8cCe7 mus musculu
Q8t2x1 mus musculu
Q1426 homo sapien
Q8wyv0 homo sapien
Q78y19 brachydanio
Q90836 gallus gall
Q9bg6 oryctolagus
Q9bg6 oryctolagus
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Q9wyf5 mus musculu
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Copyright (c) 1993 - 2004 Compugen Ltd.
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5: pl_invertebrate:*
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5: sp_mhc:*
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ALIGNMENTS

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1026 QQGFFCPEPTPGAGGTAHRRHKSSSTRNGGGELTLGLEPSEEEPPKSPLAPSEGAGSDVF 1085
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846 AARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESIPPRRFTHQSDVW 905
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"Androgen-Dependent Mammary Carcinogenesis in Rats Transgenic for the
"Androgen-Dependent Mammary Carcinogenesis in Rats Transgenic for the
"Androgen-Dependent";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AV116182; AAM50093.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:000506; F:epidermal growth factor receptor activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

GO; GO:0007169; P:transferase activity; IEA.

GO; GO:0007169; P:transferase receptor protein tyrosine kin. .; IEA.
                                                                                                       SYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECR
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Prodom; PD000001; Prot kinase;
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYRKC; 1.
PROSITE; PS00018; EF_HAND; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 TTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLID 204
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306 TDVGSCTLVCPLNNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFA 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                          6 WCRWGLLIALLPSGAAGTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELLYL 65
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                                                                                                                                                                                                                                                                                                                                                                                                           25 WLDRSVLAKELARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYL
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                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                      Length 1259;
                            ProDom; PD000001; Prot. Kinase; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TyrKc; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00107; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE DOM; 1.

ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.

SEQUENCE 1259 AA; 137989 FW; E37364D49C4ACD46 CRC64;
                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                   69.8%; Score 2136; DB 6; 36.9%; Pred. No. 5.6e-155; iive 22; Mismatches 47;
     PRINTS; PR00109; TYRKINASE
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Matches
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Mon Sep 13 07:41:05 2004

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 9, 2004, 12:20:54; Search time 10.3528 Seconds (without alignments) 2836.691 Million cell updates/sec Run on:

US-09-821-883-3 3062 1 MRAAPLLLARAASLSLGFLF.......ENPEYLGLDVPAAAHHHHH 564 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ption	1			gallus gall		homo sapien		mus musculu	homo sapien			-	-	branchiosto	-		drosophila		_	Iymnaea sta	-						mns musculu	rattus norv		homo	homo	homo	mus musculu
	Description	P04626	P06494	060553	P13387	Q15303	P00533	062956	001279	P21860	062799	P13388	P04412	P24348	002466	P70424	025197	P09208	P06213	P15208	025410	Q9wt14	P15127	P14616	P14617	P08069	P24062	060751	064716	093105	P15309	014686	P23246	P81122
SUMMARIES	ID	ERB2 HUMAN	ERB2 RAT	ERB2 MESAU	EGFR CHICK	ERB4_HUMAN	EGFR_HUMAN	ERB4 RAT		ERB3_HUMAN	ERB3_RAT		EGFR_DROME	LT23_CAEEL	ILPR_BRALA	ERB2_MOUSE	HTK7_HYDAT	INSR_DROME	INSR_HUMAN	INSR_MOUSE	MIPR_LYMST	IRR MOUSE	INSR_RAT	IRR_HUMAN	IRR_CAVPO	IGIR HUMAN	IG1R_RAT	IG1R_MOUSE		INSR AEDAE	PPAP_HUMAN	MLL2_HUMAN	SFPQ_HUMAN	IRS2_MOUSE
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	Length	ן ה			703			-			1339									1372								Н		_		5262		1321
d	Query Match	78.9	64.0	63.6	24.6	23.6	23.5	23.5	23.4	22.8	21.8	21.3	17.6	13.2	10.4	9.8	0.6	6.8	8.4	8.2	8.2	8.2	8.1	8.1	8.1	7.8	7.7	7.7	7.5	6.9	5.5	5.1	5.0	4.8
	Score	2417	1959	1946.5	752	723.5	719.5	719.5	717.5	697	668	651	539.5	404.5	318	301.5	276.5	271	258	252.5	252	251.5	249	248.5	246.5	238.5	236.5	234.5	228.5	207	168	LO.	S	148.5
	Result No.		7	٣	4	ß	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

D54951 mus musculu D9nj15 branchiosto D90534 avian leuko D92793 homo sapien D14162 homo sapien D10381 mycobacteri D10381 mycobacteri D13983 nicotiana t D13983 nicoti
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SM6B MOUSE PCK5_BRACL ERBB ALV CRB HUMAN SREG_HUMAN ODO2_MYCTU EXTN_TOBAC MI 13 HUMAN SRC2_MOUSE CC01_CAEEL
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141. 140. 139. 139. 136. 135.5 134.55. 130.5
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#### ALIGNMENTS

RESULT 1  SERIC ERRES  AC P0462  AC P0462  AC P0462  BCRES  BOT 13-AU  DT 13-AU  DT 13-AU  DT 13-AU  DT 13-AU  DE RRES  COC BUKAR  RAP COUSS  RAP SEQUE  RAP COUSS  R
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256 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHFNHSGICELECPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSASII- 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 LPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 DIQEVQGYVLIAHNQVRQVPLQRLRIVKGTQLFEDNYALAVLDNGDFLNNTTPVTGASPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ
                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
) (BY SIMILARITY).
) (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I -> V (in allele B3; dbSNP:1801201).
/FTId=VAR 004077.
I -> V (in allele B2 and allele B3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels 718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1255 AA; 137909 MW; 39E9DFDA04DCF962 CRC64;
ATP (BY SIMILARITY).
BY SIMILARITY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2417; DB 1;
Pred. No. 9.8e-138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W -> C.
/FTId=VAR 016317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTIG=VAR_004078.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I -> V (in al.
dbSNP:1801200)
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                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .; TAS.
                                  Lyrosine phosphate.

-- SUBUNIT: Heterodimer with each of the other ERBB receptors (Potential). Interacts with PRKCABP (By similarity).

-- SUBCELLULAR LOCATION: Type I membrane protein.

-- FTM: Ligand-binding increases phosphorylation on tyrosine residues (By similarity).

--- PTM: Ligand-binding increases phosphorylation on tyrosine residues (By similarity).

--- PTM: Ligand-binding increases phosphorylation on tyrosine positions 654 amilarity).

--- PTM: Ligand-binding increases phosphorylation on tyrosine residues (By similarity).

--- PTM: Ligand-binding increases phosphorylation on tyrosine residues (By similarity).

--- SIMILARITY: Belongs to the EGF receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLEASING (POTENTIAL).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0109; TYRKINASE.
Prodom; PRO0109; Prot_kinase; 1.
SMART; SM00261; FU; 4.
SMART; SM002019; TyrKc; 1.
PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
TRANSMEMBRARD; PSOUTON SMOTEIN KINASE DOM; 1.
TRANSMEMBRARD; PSOUTON SMOTEIN KINASE DOM; 1.
TRANSMEMBRARD; PSOUTON SMOTEIN KINASE DOM; 1.
TRANSMEMBRARD; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 164870; -.

R GO; GO: 0005012; F: Neu/ErbB-2 receptor activity; TAS.

GO; GO: 0004716; F: receptor signaling protein tyrosine kinase GO; GO: 0004716; F: receptor signaling protein tyrosine kinase . . .;

R GO; GO: 0007167; F: receptor signaling paction; TAS.

R GO; GO: 0007167; P: protein amino acid dephosphorylation; TAS.

GO; GO: 0006480; P: protein amino acid dephosphorylation; TAS.

InterPro; IPR00641; Furin-Tike.

R InterPro; IPR00621; Furin-Tike.

R InterPro; IPR006212; Furin repeat.

InterPro; IPR006212; Furin repeat.

InterPro; IPR006212; Furin repeat.

InterPro; IPR006125; Furin repeat.

InterPro; IPR006125; Furin repeat.

InterPro; IPR006125; Furin repeat.

InterPro; IPR006125; Furin repeat.

InterPro; IPR001465; Tyr_pkinase.

InterPro; IPR001465; Tyr_pkinase.

InterPro; IPR0014019; YIP_motif.

R Pfam; PP00757; Purin-Like; 1.

R Pfam; PP00757; VILI-Like; 1.
       alpha and amphiregulin.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AY208911; AA018082.1; -.
EMBL; X03363; CAA27060.1; -.
PIR; A24571; A24571.
PDB; 1N8Z; 18-FEB-03.
PDB; 1QR1; 01-JAN-00.
Genew; HGNC:3430; ERBB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism; 3D-structure SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
DOMAIN
TRANSMEM
DOMAIN
NP_BIND
```

94



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OM protein - protein search, using sw model

0; Search time 18.0048 Seconds (without alignments) 3013.200 Million cell updates/sec 9, 2004, 12:29:10 September Run on:

US-09-821-883-3 3062 Title: Perfect score:

1 MRAAPLLLARAASLSIGFLF........ENPEYIGLDVPAAAHHHHH 564 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
-	2417	78.9	1255	н	A24571	protein-tyrosine k
8	1962	64.1	1260	Н	TVRTNU	protein-tyrosine k
m	1946.5		1254	7	148161	ă
4	752	24.6	1223	-	TVCHLV	epidermal growth f
ហ	751		527	7	A42032	_
9	723.5	23.6	1308	7	A47253	_
7	719.5	23.5	1210	Н	GOHUE	_
80	717.5	23.4	1210	~	A53183	l growth
0	713.5	23.3	644	~	A36325	_
10	697	22.8	1342	~	A36223	н
11	662	21.6	1339	~	JC4387	epidermal growth f
12	651	21.3	1166	Н	S06142	yrosine
13	539.5	17.6	843	~	A27131	epidermal growth f
14	404.5	13.2	1323	~	E88257	protein let-23 (im
15	404.5	13.2	1374	7	S70712	protein-tyrosine k
16	390.5	12.8	1369	8	870713	protein-tyrosine k
17	379	12.4	1330	Н	GOFFE	l growth
18	341	11.1		7	D45558	l growth
19	341	11.1	-	Н	A45558	_
20	331	10.8		~	B45558	epidermal growth f
21	331	10.8	342	7	C45558	_
22	318	10.4	1363	7	T43220	insulin-like growt
23	276.5		1477	7	T18534	protein-tyrosine k
24	271	8,9	2101	~	S57245	insulin receptor (
25	271		2148	-	A56081	
26	258		1382	ч	INHUR	
27	252.5		1372	7	A34157	insulin receptor p
28	252	8.5	1607	~	T43212	
29	249	8.1	1383	~	A36080	insulin receptor p

30 246.5 8.1 1300 2 A36502 31 238.5 7.8 1367 1 IGHURI 32 236.5 7.7 1371 2 A33837 34 233.5 7.7 1371 2 A33837 35 231.5 7.6 1268 2 B47417 36 224.5 7.3 139 2 A48805 37 207 6.8 1390 2 T30346 38 188 6.1 1846 2 T42047 41 153.5 5.0 707 2 A46305 42 146 4.8 351 2 S50754 43 139.5 4.6 597 2 S72468	insulin receptor-r insulin-like growt insulin-like growt	tyrosine kinase re insulin receptor-r insulin receptor-r insulin-like growt	insulin receptor - insulin receptor h acid phosphatase ( ALR protein - huma	PTB-associated spl hypothetical proce cell wall glycopro hypothetical prote	probable transcrip
87777777777777777777777777777777777777	A36502 IGHUR1 A33837	JH0803 B47417 B36502 A48805	T30346 T42047 JH0610 T03454	A46302 S50754 S50062 S50755	872468
87777777777777777777777777777777777777	212	0000	2242	00000	7
	1300 1367 1371	183 540 1268 329	1390 1846 386 5262	707 351 442 473	287
30 246.5 31 238.5 32 236.5 33 235.5 34 233.5 36 234.5 36 234.5 37 201.5 38 188 40 188 41 133.5 45 139.5	8.1 7.8 7.7	7.7.7.	6.0.0.0 6.1.0.1	0 8 8 6	4.
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	30 31 32	6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	788 786 04	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	2.

### ALIGNMENTS

A; Reference number: A2471; WID:8611863; PMID:3003577
A; Reference number: A2491; WID:86016729; PMID:295567
A; Reference number: A2491; WID:86016729; PMID:295994
A; Reference 20, 1132-1139; 1936
A; Residues: 737-1031 c88N
A; Residues: A37-1031 c88N
A; Residues: A44188
A; MID:86070181; PMID:299994
A; Reference 20, 1132-1139; 1936
A; Residues: A44188
A; MID:86070181; PMID:299994
A; Residues: A44188
A; MID:86070181; PMID:2999994
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A; MID:86070181; PMID:2992089
A; Residues: A44188
A; MID:86070181; PMID:86070181
A; Reference number: A44188
A; MID:86070181; PMID:39929; MID:87286898; PMID:309351
A; Residues: A299; A9476
A; Reference number: A44188
A; MID:87286898; PMID:3093951
A; Residues: A7478
A;

A;Cross	-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332 nt. Amnlification and overexpression of this erb8-related gene occurs in about 30	q	616 FPDEEGACQPCPINCT
C, Genet		λo	334
A; Gene: A; Cross	UDS:ERBEZ, NGL; NEU; NEU; NEU; NEU; NEU; NEU; NEU; NEU	Db	676 KRRQQKIRKYTMRRL
A; Map p	OBILION: 1/421.1-1/421.1 ns: 25/1; 75/3; 147/1; 883/3	۵	334
C; Funct		Ор	736 KGIWIPDGENVKIPV,
A;Descr C;Super C;Keywo	A;DeBGIDTION: CAGALYZEB TONE DIOSPINOTYLATION OL A PEPLICY LYIOSINE FEBILUE DY ALF C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Reywords: ATP; autophosphorylation; duplication; qlycoprotein; phosphoprotein; phospho	ò	334
inase		qa	796 LVTQLMPYGCLLDHVF
F;1-21/ F;22-12	Domain: signal sequence #Status predicted <51G> 55/Product: protein-tyrosine kinase erbB2 #Status predicted <mat></mat>	٨٥	334
F; 24-65 F; 70-30	i <eal></eal>	Db	856 PNHVKITDFGLARLLI
F;395-6 F;654-6	nain repeat ed <tmm></tmm>	λō	334
F;676-1 F;718-9	255/Domain: intracellular #status predicted <int> 83/Domain: protein kinase homology <kin></kin></int>	qq	916 MTFGAKPYDGIPAREI
F;726-7 F;68,12 E:66/B	34/Region: protein Kinase Air-Dinding Motii 4.187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predict indian site: phosphate (Mbr) (covalent) (by protein binase C) #status predicted	ò	339
F;753/A F:753/A	'yr) (cowalent) (by an	DP	976 FSRMARDPQRFVVIQN
, , , , , , , , , , , , , , , , , , ,	71) (coracina) (2)	λō	339GAGGMVHHRHRSS
Best		Db 1	1036 APGAGGMVHHRHRS
		λo	397 KGLQSLPTHDPSPLQE
දු ද	35 LARGAASTQVCTGTDMKLREPASPETHLDMLKHLYQGCQVVQSNLELITLFITASLSFLQ 94 16 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	Db 1	
8 8	DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLANTTPVTGASPG 1		
q <sub>0</sub>		<b>.</b>	
ò	155 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC 214		
q	136 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC 195	Db 1	1216 AFDNLYYWDQDPPERU
ò	215 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC 274	RESULT 2	
QQ	196 SPWCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPRHSDCLAC 255	protein-ty	protein-tyrosine kinase (EC 2
ò	275 LHFNHSGICELHCPALVTYNTDIFESMPNPBGRYTFGASCVTACPYNYLSTDVGSASII- 333	C;Date: 31 C;Accession	C, Decree: Marcas Morvegrass C, Date: 31-Dec-1988 #sequence C: Accession: A24562; A61204
qq	256 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC 315	R; Bargmann,	, C.I.; Hung, M.C.;
ò	334 333	A,Title: T	he neu oncogene enc
Οp	316 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 375	A; Accession	n: A24562
ò	334 333	A;Residues	: 1-1260 <bar></bar>
QQ	376 FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI 435	A; Masui, T	A; Cross-references: EmbL: AU333 CR: Masul, T.; Mann, A.M.; Macat
δ	334 333	A, Title: D	irect DNA sequencin
Dp	436 LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 495	A, Reference	e number: A61204; N
ò	334 333	A;Status:	A, Moleculary A, Moleculary A, Moleculary
q	496 TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGGECVEECRVLQGLPREYV 555	A;Residues	1 637-663,'V',665-7
ò	334 333	C, Genetics	cilors cranstaced cil
QQ	556 NARHCLPCHPECQPQNGSVTCFGPBADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615	C, Superfamily:	ily: epidermal growt
ò	334 333	F;1-19/DOM	Circywolds: Air; aucophosphor; F;1-19/Domain: signal sequence
		F;20-1260/	Product: protein-ty

3362; NID:956745; PIDN:CAA27059.1; PID:956746
2atee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen, 3, 1991
Ing of the rat neu oncogene transmembrane domain reveals no methyl.N-nitrosourea.
MUID:92035293; PMID:1682063 C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho F;1-19/Domain: signal sequence #status predicted <SIG> F;20-1260/Product: protein-tyrosine kinase neu #status predicted <NAT> codes an epidermal growth factor receptor-related protein. WIID:86118662; PMID:3945311 QRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPBSPREG 456 AKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP 516 ONEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP 1035 CTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVLGVVFGILI 675 LLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 735 VAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ 795 VRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS 855 ----- 333 LDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 915 1 : 1 SIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE 975 - 338 SSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA 396 2.7.1.112) neu precursor - rat (Norway rat) e\_revision 31-Dec-1988 #text\_change 11-Jun-1999 ----NEEKL---702 <MAS> he codon GCA for residue 25 as Val RGAPPSTFKGTPTAENPEYLGLDVP 555 ; Weinberg, R.A.



Sequence 126, App Sequence 1, Appli Sequence 2, Appli Sequence 6, Appli Sequence 3, Appli

US-10-435-696-36 US-10-441-779C-4 US-10-734-564-126

Sequence 53, Apples Sequence 3, Appli Sequence 45, Appli Sequence 15, Appli Sequence 17, Appli Sequence 68, Appli Sequence 68, Appli Sequence 14, Applesquence 118, Applesquence 118, Applesquence 5, Appli Sequence 5, Appli

Sequence 11, App) Sequence 7, Appli

ALIGNMENTS

Sequence 13, App.

479 645

64.1 64.1 64.0 60.0 52.7 52.7

Sequence 13, Ap Sequence 3, Ap

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US-09-821-883-3
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 September 9, 2004, 12:41:37; Search time 59.6409 Seconds (without alignments) 3032.635 Million cell updates/sec
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| cgn2 6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| cgn2 6/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*
| cgn2 6/ptodata/2/pubpaa/US06_PUBCOMB.ppp:*
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| cgn2 6/ptodata/2/pubpaa/US08_NEW_PUB.ppp:*
| cgn2 6/ptodata/2/pubpaa/US08_NEW_PUB.ppp:*
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| cgn2 6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
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(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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                                   Copyright
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121 VRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQL 180
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Sequence 3, Application US/09821883
Fatent No. US2002061310A1
FAPLICANT: LAUS, Reiner
APPLICANT: LAUS, Reiner
APPLICANT: Gradis, Thomas
TITLE OF INVENTION: Cempositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
FRIOR PILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: HER500* construct
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 6, Appli Sequence 2, Appli Sequence 4, Appli Sequence 28, Appl Sequence 594, App

US-09-984-092-4 US-10-177-293-126 US-10-207-498-6 US-10-338-730-2 US-10-322-892-4 US-10-272-437A-28 US-10-117-937-594

Sequence 2, Appli Sequence 6, Appli Sequence 3, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 126, Appli

US-09-821-883-1 US-09-821-883-2 US-09-854-356-6 US-09-811-123-9 US-09-811-115-3 US-09-811-115-3

Sequence 3, Appli Sequence 4, Appli

Sequence 1 Sequence

Description

Appli

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MPNPEGRYTFGASCVTACPYNYLSTDVGSASIINFEKLGAGGMVHHRHRSSSTRSGGGDL 360
                                                                                                                                                                                                   TLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 420
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                    CYODIILWKDIFHKNNOLALTLIDINKSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA
                                                                    GGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFES
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APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REPERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION: HER500 construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/09821883
; Patent No. US20020061310A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       541 TPTAENPEYLGLDVPAAA 558
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LENGTH: 555
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61 HLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRI 120
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                                                                       CYODIILWKDIFHKNNOLALTLIDINRSRACHPCSPWCKGSRCWGESSEDCOSLTRTVCA
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                                                                                                                                                                                                                                                                                                                                          HIDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRI
                                                                                                                   GGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFES
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Fatent No. US20020061310A1

GENERAL INFORMATION:

APPLICANT: Laus, Reiner

APPLICANT: Graddis, Thomas

ITTLE OF INVENTION: Cell-Based Immunotherapy

FILE REFERENCE: 758-6-0022.30

CURRENT APPLICATION NUMBER: US/09/821,883

CURRENT FILING DATE: 2001-03-30

PRIOR PILING DATE: 2000-03-30

PRIOR FILING DATE: 2000-03-30

SOFTWARE: FASELSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH...697
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Sequence 7, Appli

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September 9, 2004, 12:31:25; Search time 16.4294 Seconds (without alignments) 1772.256 Million cell updates/sec
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1 MRAAPLLLARAASLSLGFLF.......ENPEYLGLDVPAAAHHHHH 564
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Copyright (c) 1993 - 2004 Compugen Ltd.
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. 60	2417	78.9			US-08-356-786-2	Sequence	2	App]
σ	2417	78.9			US-08-466-680B-68	Sequence	68,	Apr
10	2417	78.9		•	US-09-354-533-68	Sequence	68,	Apr
11	2397				US-08-484-438-8	Sequence	8	App]
12	1614.5				US-09-146-283-4	Sequence	4	App1
13	1614.5			М	US-08-579-823A-4	Sequence		App]
14	1614.5			m	US-09-344-195-4	Sequence	4	App]
15	1610.5			4	US-09-630-155-2	Sequence	7	App]
16	1599.5			٣	US-08-422-108-1	Sequence	Ä	App]
17	1599.5			4	US-08-422-734-1	Sequence	ä	App]
18	1177			Н	US-08-414-417B-69	Sequence		Apr
19	1177					Seguence		App
20	1177				US-08-468-545B-69	Seguence		Apr
21	1177	38.4		٣	US-08-466-680B-69	Seguence	69	App
22	1177	38.4			US-09-354-533-69	Sequence		Apr
23	860	28.1			US-09-648-067A-1	Sequence	'n	App]
24	723.5	23.6	911	7	US-08-484-438-10	Sequence	10,	Api
25	723.5	23.6	_		-08-484			App]
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27	719.5	23.5		-	US-08-336-708A-9	Seguence	6	Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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	ò		215	SPMCKGSRCWGES	RCWGESSI	ပ္ထို	SSEDCOSLTRTVCAGGCAR	AGGCA	RCKGPLPTDCCHEQCAAGCTGPKHSDCLAC	CAAGCTGPKH	SDC		274
	q		196	SPMCKGS	RCWGESSI	- <u>ŏ</u>	SLTRTVC	AGGCA	RCKGPLPTDCCHEC	CAAGCTGPKH	SDC	LAC 2	25
	ò		275	LHFNHSG	ICELHCPA	3	YNTDTFE	SMPNP	EGRYTFGASCVTAC	PYNYLSTDVG	SAS	11- 3	33
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                                                                                                             Indels 718;
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                                                                                Score 2422; DB 4;
Pred. No. 1.3e-187;
4; Mismatches 5;
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Best Local Similarity 41.3
Matches 512; Conservative
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; ORGANISM: Homo
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Patent No. 6552979

GENERAL INFORMATION:
APPLICANT: ETICKSON, Sharon
APPLICANT: Schwall, Ralph
APPLICANT: King, Kathleen
TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
FILE REFERENCE: GENENT: 034A
CURRENT APPLICATION NUMBER: US/09/811,115
CURRENT PILLING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/189,844
PRIOR APPLICATION NUMBER: 60/189,844

PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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* ×	N-FSDB; AAUZIS66.
<u> </u>	An immunostimulatory fusion protein comprising the intracellular domain
L L	of HER-2 and an antiden elicits an immune response to the antigen and is
PT	useful for the treatment of associated cancer associated.
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PS **	Claim 7; Page 26; 59pp; English.
<b>4</b> E	The invention relates to imminisation fusion proteins (IPP) and
38	
ខ	polypeptide antigen component and an immunostimulatory component derived
႘	from the intracellular domain of HER-2 protein which is effective to
ខ	elicit a protective dendritic cell (DC) - induced T-cell mediated cellular
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Query Match

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Aae13110 Human HER Aae13109 Human HER Aae13109 Human HER Aab21203 Human HER Aab51203 Human HER Aay51400 Human HER Aae2636 Human HER Aae2636 Human HER Ab747447 Beest ca Ab74747 Beest ca Ab74747 Beest ca Ab74747 Beest ca Ab74747 Beest ca Ab77255 Human Erb Ada7255 Human HER Ada88866 Human HER Aay84780 Amino aci Aab676198 Human HER Aab88866 Human HER Aab88866 Human HER

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AAW01111 AAW92406 AAY84780 AAB21198

AAG88267 AAB85458 AAE20479

ABR47447 ABP74708 AAE38390

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used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular domain, an Ala linker, an ovalbumin (OVA)-derived immunodominant octapeptide, HER-2 membrane distal
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                                                                                                                                                                Score 3062; DB 4;
Pred. No. 1.8e-211;
Mismatches 0;
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The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 rGM-CSF fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular domain, an Ala linker, an ovalbumin (OVA)-derived immunodeminant octapeptide, HER-2 membrane distal intracellular domain, an Ala linker, a mature rat granulocyte-macrophage colony stimulating factor (GM-CSF) sequence and a
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Pred. No. 6.7e-208;
0; Mismatches 0;
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100.0%; Pre
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                 Copyright
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- nucleic search, using frame\_plus\_p2n model OM protein

September 10, 2004, 05:57:41; Search time 4652.68 Seconds (without alignments) 4428.608 Million cell updates/sec Run on:

Title: Perfect score:

US-09-821-883-2 3739 1 MRAAPLLLARAASLSLGFLF......EPVQEGAPPPPAAAHHHHH 690 Sequence:

Scoring table:

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** 

27513289 segs, 14931090276 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODBL=frame+ p2n.model -DEV=xlh
-MODBL=frame+ p2n.model -DEV=xlh
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-DS=21/USFYO\_spool/USG09821883/runat\_09092004\_105127\_6643/app\_query.fasta\_1.3100
-DS=EST -QFWT=fastap -SUPFIX=rsf -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=b1ts -GTART=1 -END=-1 -MATRIX=b100=um62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNFRY=pct -NORM=ext -HEAPSIZE=500 -MINITSN=0 -MAXLEN=2000000000
-USER=USG9821883\_@CGN 1 1 11571\_@runat\_09092004\_105127\_6643 -NCPU=6 -ICPU=3
-NOW MAAP -LARGEQUERY -NGG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database

em\_estpl:..
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# 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	K031099 Mus mu	52913 AGEN	02792	55074	88274	183	55141	131	CDSISSS AGENCOURT	1340 OFFI	1931	1765 D	14 DKFZp68	W- I :	2	4	CD/ZIBOI OJOIEO/.y	200	3 Mus	980 AGEN	797	283	693	872	CB598701 AGENCOURT	222	45/0 AGENCO	187	37981	342	BG283493 602407782	97	155788 602904	Z ZV37802	520 685491	77542 ux45d0	0012 RC-BT105	69889 U		98814 0	55157 60	
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### ALIGNMENTS

AK031099 LOCUS DEFINITION RESULT 1

AK031099

Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930404N10 product:verb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog 1, neuro/glioblastoma derived homolog (avian), full insert sequence.

ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

AK031099
AK031099.1 GI:26082143
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayatau, N., Hirozane, T., Hari, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sakazume, N., Sogabe, Y., Tangami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                       Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normanization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sawi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watsuhiki, M., Ohada, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4323)
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                    cloning
                                                             Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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neuro/glioblastoma derived oncogene homolog (avian)
(MGD|MGI:95410, GB|U71126, evidence: BLASTN, 99%,
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/clone_lib="RIKEN full-length enriched
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Matches:
Conservative:
Mismatches:
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xref="FANTOM_DB:5930404N10"
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                                                                                 /dev stage="13 days embryo<sup>*</sup>
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Please visit our web site for further details

URL: http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/ Location/Qualifiers

.4323

PEATURES

/organism="Mus musculus" /mol\_type="mRNA" /strain="C57BL/6J"

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-MODEL=frame+ p2n.model -DEV=xlh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3739
1 MRAAPLLLARAASLSLGFLF......EPVQEGAPPPPAAAHHHHH 690
                                                                                                                                                                                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                        - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3304383 segs, 2515761380 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications_NA:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
Mon Sep 13 07:41:01 2004
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

sult Query No. Score Match Length DB Result

Description

1,0,0,0	, 11, e	Sequence 45, Appl Sequence 11, Appl Sequence 125, App		equence 1	9 6	9	Sequence 10, Appl Sequence 59, Appl	Sequence 1	Sequence ', Appii Sequence 1, Appli	u,	m -	שינ	Sequence 5	ω` r	Seguence 3,	9	Sequence 3,	Sequence 9, Appli Sequence 1, Appli	Sequence 1,	٠, د د د د	Ì.	equence 117,	10,	Sequence	11,	equence 3,	Sequence 5, Appli	quence 2
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### ALIGNMENTS

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APPLICANT: Laus, Reiner
APPLICANT: Uidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT PILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: HER500-hGM-CSF construct
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 2070
                     Sequence 7, Application US/09821883
Patent No. US20020061310A1
GENERAL INFORMATION:
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US-09-821-883-7
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Mon Sep 13 07:41:01 2004

Page 2

US-09-821-883	1-883-7					Ę	
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Best Loca	al Similarity:	100.00%		00		è	
DB:	:	50.00	daps:	) O		; A	1021 AGCTCATCTACC
US-09-821-883	1-883-2 (1-690)	x US-09-821-883	33-7 (1-2070)			l è	361 Gluala Proare
È	1 MetArgAla	AlaProLeuLeuLeu	Maargalaalase:	MetArgAlaAlaProLeuLeuLeuAlaArgAlaAlaSerLeuSerLeuGlyPheLeuPhe	20	S &	
qa	1 ATGAGAGCT	rgcaccccrccrccrc	3GCCAGGGCAGCAAG		09	š	
ò	21 LeuLeuPhe	PheTrpLeuAspArc	ySerValLeuAlaLy	euLeuPhePheTrpLeuAgpArgSerValLeuAlaLysGluLeuAlaArgGlyAlaAla	40	; f	1141 GACCTGGGAATG
Db	61 CTGCTTTT	rttctggctagaccg	AGTGTACTAGCCAA		120	}	2111222 Ga [ Direct 104
ò	41 SerThrGln	ValCysThrGlyTh	rAspMetLysLeuArd	erThrGlnValCysThrGlyThrAspWetLysLeuArgLeuFroAlaSerProGluThr 6	09	÷ 8	1201 CTACAGGGTAC
qq	121 rcgacccaa	Agrecaccecac	AGACATGAAGCTGCG		180	ò	
ζó		OMEtLEUArgHisLeu	1TyrGlnGlyCysGl	HisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeuGlu	80	: 쇰	
qq	181 CACCTGGAC	cardedeceden	craccaddecrecca		240	ò	441 ProProSerPro
ò		rLeuProThrAsnAla	aSerLeuSerPheLe	LeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluValGln 1	100	qq	1321 CCCCCTTCGCCC
DÞ	241 CTCACCTAC	cergeceaecaarge	SAGCCTGTCCTTCCT	CAGGATATCCAGGAGGTGCAG 3	300	ò	461 ArgAlaLysThr
ò		LeulleAlaHisAsr 		GlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg1le	120	q	 1381 AGGCCAAGACT
qq	301 GGCTACGTG	SCTCATCGCTCACAAC	CCAAGTGAGGCAGGT		360	à	481 GlyAlaValGlu
ò		ThrGlnLeuPheGlu	<b>.МврАвпТугА]</b> аLе 	ValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGlyAsp	140	qq	
q	-	CACCCAGCTCTTTGAC	3GACAACTATGCCCT(	GCCGTGCTAGACAATGGAGAC 4	420	ò	501 ProproproAla
λo		JASNThrThrProVa]	ThrGlyAlaSerPro 	ProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeuGln 1	160	ΟD	1501 CCTCCTCCTGCC
QQ	421 CCGCTGAAC	SAATACCACCCCTGTC	zacadedecricece		480	à	521 GluArgGlyAla
ò	161 LeuArgSer	rLeuThrGluIleLer	1LysGlyGlyValLe1	LeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGlnLeu	180	qq	
Ω <b>p</b>	481 CTTCGAAGC	CCTCACAGAGATCTTC	Baaaggaggtctt		540	ò	541 LeuGlyLeuAsp
Š		148pThr1]eLeuTr 	oLysAspIlePheHi 	CysTyrGlnAspThr11eLeuTrpLysAsp11ePheHisLysAsnAsnGlnLeuAlaLeu	200	qq	 1621 CTGGGTCTGGAC
Ор	541 TGCTACCAG	SGACACGATTTTGTGC	Baaggacatcttcca		009	ò	561 TrpGluHisVal
ò		eAspThrAsnArgSe	rArgAlaCysHisPro	ThrieuileAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLy8Gly ?	220	qa	 1681 TGGGAGCATGTG
සු		AGACACCAACCGCTCT	rcgggccrgcccAccc		099	ò	581 AlaAlaGluMet
è 1		STrpGLyGluserses		SefArgCyglrDGJVGIUSESSETGIUASDCY8GJINSETLeUINFATGINFYAICY8FATA 	220	qq	1741 GCTGCTGAGATG
g ¿			IGAGGAIIGICAGAG		07/	ò	601 ThrCysLeuGlr
े द		3A14A19Cyshysg1)			0 00	qq	1801 ACCTGCCTACAG
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<b>∂</b> 8		GAGCTGCACTGCCC		GIVITEC VOLUMENTS SYSTEMATER VALUE AND THE STANDARD STAND	006	qq	1921 GAAACTTCCTGI
} {			100 c [ W. [ Do 40 - 40 - 40 - 40 - 40 - 40 - 40 - 40		330	ò	661 PheLeuLeuVal
ò	301 MetProAsn	ıProGluGıyArgıyı	rThrPheGiyAlase	MetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysProTyr :	320		- - - - - - - - - - - - - - - - - - -

Sequence 1, Appli Sequence 26, Appl Sequence 25, Appl Sequence 3, Appli Sequence 17, Appl Sequence 7, Appli Sequence 7, Appli Sequence 3, Appli

Appl Appli Appli Appli Appli Appli Appli Appl

Sequence Sequence Sequence

Sequence

Appli Appli Appli Appli

Sequence 1, Sequence 3,

Patent No. 5200327 Sequence 9, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

Sequence 6 Sequence 6 Sequence 6

Sequence Sequence

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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APPLICANT: RAZIUDDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: BRBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 30303

ZIP: 30303

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
US-09-146-283-3

US-08-579-823A-3

US-08-229-515A-14

US-08-422-108-2

US-08-422-108-2

US-08-422-108-2

US-08-422-108-2

US-09-146-283-1

US-09-146-283-1

US-09-146-283-1

US-09-146-283-1

US-09-146-283-1

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US-09-658-883B-1

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US-09-676-610B-25

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US-08-484-438-1

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US-08-3118-193-3

US-08-3118-193-3

US-08-3118-193-3

US-08-3118-193-3

US-08-3118-193-3

US-08-3118-193-3

US-08-484-438-1

US-09-118-69-3
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PILING DATE: 19 APR 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PEREXYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/POCKET NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELECHONE: 404-688-9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 9, Application US/08229515A; Patent No. 5518885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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                                                 CITY: Atlanta
STATE: Georgia
COUNTRY: usa
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199.23333
                                                                                                                                          US-08-229-515A-9
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1647
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-FGAPEXT=7 -YGAPPOP=10 -YGAPEXT=0.5 -DELOPEG -DELEXT=7
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6: /cgn2_6/ptodatc/lina/PcTUS_COMB.seq:*
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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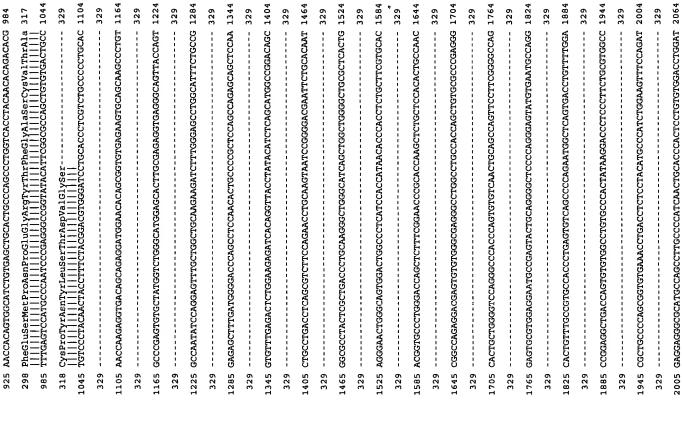
200432

Score

Result

Database :

, t	cid	QQ	925 AACCACAGTGGCATCTGTGAGCTGCACTGCCCAGCCCT
	STRANDEDNESS: single TOPOLOGY: linear	ò	298 PhegluSerMetProAsnProGluGlyArgTyrThrPh
US-08-22		ΩÞ	CCCAATO
Alignmen Pred. No		ò	318 CysProTyrAsnTyrLeuSerThrAspValGlySer
Percent		Ωp	1045 TGTCCCTACAACTACCTTTCTACGGACGTGGGATCCTG
Query Ma	64.80% Indels:	ò	329
US-09-821-883-2	0) x US-08-229-515A-9 (1-4530)	QQ	1105 AACCAAGAGGTGACAGCAGGAGGATGGAACACAGGGGTG
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<u></u>	2 Atgatanteroleureureurantyna	qq	1165 GCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCG
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g (	GAGCIGGCCCITGTGCCGCTGGGGGCTCCTCGCTCGCCCCTCTTGCCCCCCCC	ò	329
දු දි	38 GIVALAALASSETIITGIINVALCYSTITGIIVIITTABDMEELVSDENAIGLEUKIOALASSET 5/ 208 GIAGOOGGGAGOOAGGGGGGGGGGGGGGGGGGGGGGGGG	ДQ	1285 GAGAGCTITGAIGGGGACCCAGCCTCCAACACTGCCCC
i i	Description of subsequents on a conference of suffered and afternoon and afternoon of suffered by a 10 a 1	ò	329
Š 1	FIGURE SECTION STREET SECTION OF	Dp	1345 GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATA
<b>Q</b> O	CCCGAGACCCACCTGGACATGCTCCGCCACCTCTACCAGGGCTGCCAGGTGGTGGAGGAA	ò	329
∂ ්	AsnLeudluLeuThrTyrLeuProThrAshAlaserLeuSerPheLeudlhasplieGin	Dp	1405 CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAAT
<b>Q</b> II	AACCIGGAACICACCIACCIGCCCACCAGACIGCCIGICCIGCAGGAIAICCAG	ò	329
ð i	GluvalGlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArg	οp	1465 GGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATCAG
QQ	GAGGTGCAGGGCTACGTGCTCATCGCTCACAAGTGAGGCAGGTCCCCACTGCAGAGG	ò	329
ð 1	LeuArg1leValArgG]YThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAsp 	Dp	1525 AGGGAACTGGGCAGTGGACTGGCCCTCATCACATAA
<u>a</u>	CIGUGGAITUSTGCGAGGCCCCGGCTCTTTGAGGACAACTATGCCCTGGCCGTGCTAGAC	ò	329
ð í	AsnGlyAspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArg	qq	1585 ACGGIGCCCTGGGACCAGCTCTTTCGGAACCCGCACCA
qq	AATGGAGACCCGCTGAACAATACCACCCCTGTCACAGGGGCCTCCCCAGGAGGCCTGCGG	ò	329
ð t	158 GluLeuGlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsn 177	ορ	1645 CGGCCAGAGGACGAGTGTGGGCGAGGGCCTGGCCTG
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රු දි	178 ProGineucystyrcinapinilleleuirplysaspilePhenislysashangin 197 	QQ	1705 CACTGCTGGGGTCCAGGCCCCACCCAGTGTGTCAACTG
ìò	LeualaleuThrLeuIleAspThrAsnArqSerArqAlaCysHisProCysSerProMet	ò	329
n &		ΩP	1765 GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCC
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Š 1		Db	1885 CCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAA
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<b>∂</b> 8	258 GITTY BALLATIA GALLY CABLITATIVE PER BALBOSETABLY SERVICE CALLATARIA GALLATARIA GALL	DP	1945 CGCTGCCCAGCGGTGTGAAACCTGACCTCTCCTACAI
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Scoring table:

Total number

Searched:

Minimum DB Maximum DB

Perfect score:

Sequence:

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Aaq46083 Adb47370

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/*tag= a // product= "Human HERS00-hGM-CSF fusion protein construct comprising human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular and intracellular domains, an Ala Ala linker, a mature human GM-CSF sequence and a C-terminal tag" // note= "CDS does not include stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunostimulatory fusion protein; IFP; antigen component; therapy; immunostimulatory component; T-cell mediated immune responses, DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; GM-CSF; HERR-2 protein; granulocyte-macrophage colony stimulating factor; HERS00-hGM-CSF fusion DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human HER500-hGM-CSF fusion DNA construct.
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 Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
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-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-DB=N Geneseq 29Jan04 -QFMT=fasterp -SUFFIX=rng -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UMITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MINLEN=0 -ALIGN=15
-MODEL-CAL. -GOTFWT=pto -NOFM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09821883 @CGN 1 1 1646 @runat 09092004 105126 6623 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPEDCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAROP=10 -XGARDEXT=0.5 -FGAPOP=6
-FGAPOR=17 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Aad21567 Human HER
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Aad21566 Human HER
Aat01585 Her-2/neu
Aar71253 Human HER
Aac0815 Nucleotid
Aad19731 Human tyr
                                                                    September 10, 2004, 05:04:16; Search time 679.537 Seconds (without alignments) 4313.608 Million cell updates/sec
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           version 5.1.6
- 2004 Compugen Ltd.
                                                 - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                           of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993
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                                                                                                                                                                                                                  The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HBR-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HBR500 hGM-CSF fusion DNA construct which comprises DNA molecules encoding human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HBR-2 signal sequence, mature HBR-2 membrane distal extracellular and intracellular domains, an Ala Ala linker, a mature human granulocytemacrophage colony stimulating factor (GM-CSF) sequence and a C-terminal
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                                                                                                                                                              An immunostimulatory fusion protein comprising the intracellular domain of HER-2 and an antigen elicits an immune response to the antigen and is useful for the treatment of associated cancer associated.
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                     GTGCGAGGCACCCTTTGAGGACAACTATGCCCTGGCCGTGCTAGACAATGGAGAC
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                  1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                         September 9, 2004, 12:28:07
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Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
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sp_virus:*
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_inverebrate:*
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sp_mamnal:*
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1: sp_archea:*
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Match ]
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Perfect score:
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1951
1609.5
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0	331 323.5 305
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### ALIGNMENTS

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n nosvi; filloci; filloci; cmembrane; IEA.

RO; GO; 0005524; F:ATP binding; IEA.

RO; GO; 0005524; F:ATP binding; IEA.

RO; GO; 0005509; F:calcium ion binding; IEA.

RO; GO; 0005500; F:calcium ion binding; IEA.

RO; GO; 0005006; F:cansferane activity; IEA.

RO; GO; 0005006; F:cansferane activity; IEA.

RO; GO; 000500648; F:transferane activity; IEA.

RO; GO; 00001699; F:transferane activity; IEA.

RICEPTO; IPR004919; EGFR L domain.

RICEPTO; IPR009109; Furin repeat.

RICEPTO; RECORD L moutif.

REam; PF001030; Recept L domain; 2.

REam; PF001030; Recept L domain; 2.

REam; PF01030; Recept L domain; 2.
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.

"CODA cloning of erbB-2 from canine mammary gland.";

"CDNA cloning of erbB-2 from canine mammary gland.";

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, AB008451; BAA23127.1;

HSSP; P11362; IFGK.
                                                                                                                                       Last sequence update)
Last annotation update)
PRT; 1259 AA
                                                                                               Created)
                                                                                     01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-OCT-2003 (TrEMBLrel. 25,
PRELIMINARY;
                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
                                             PACACA COCCOS BEACA COCCOS BEAC
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Ogerv6 mus musculu Ogwrf5 mus musculu Ogep98 mus musculu

717.5 717.5 717.5 714.5 708.5

O9qx70 rattus norv Q8mil8 sus scrofa

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STRAIN=BDIX;
Watson P.A., Kim K., Chen K.-S., Gould M.N.;
Watson P.A., Kim K., Chen K.-S., Gould M.N.;
Watson P.A., Kim K., Chen K.-S., Gould M.N.;
Watchen Dependent Mammary Carcinogenesis in Rats Transgenic for the New Proto-Oncogene.";
Submitted (WAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AVI16182; AAM50093.1; --
SR GO; GO:0016020; G:membrane; IEA.

GO; GO:0016020; G:membrane; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0006747; F:protein errine/threonine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

GO; GO:000169; P:transferase activity; IEA.

GO; GO:000169; P:transferase activity; IEA.

GO; GO:000468; P:protein amino acid phosphorylation; IEA.

GO; GO:000468; P:protein amino acid phosphorylation; IEA.

GO; GO:000468; P:protein amino acid phosphorylation; IEA.

GO; GO:000468; P:protein amino acid phosphorylation.

GO; GO:000468; P:protein amino acid phosphorylation.

GO; GO:000468; P:protein Fransferase activity; IEA.

GO; GO:000468; P:protein amino acid phosphorylation.

GO: GO:000468; P:protein amino acid phosphorylation.

GO: GO:000468; P:protein Fransferase activity: IEA.

GO: GO:000468; P:protein amino acid phosphorylation.

GO: GO:000468; P:protein Fransferase activity: IEA.

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                                                                                                                                                                                                                                                                                                                                    438
                                                                                                                                                                                                                                                                                                                                                                                                                                 493
AARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESIPPRRFTHQSDVW 905
                                                                                               SYGVTVWELMIFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMVKCWMIDSECR
                                                                                                                                                                                                                                                                                                                                    DGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVR
                                                                                                                                                                                                                                                                                                                                                                                                                               POPPSPREGPLPAARPAGATLER----AKTLSPGKNGVVKDVFAFGGAVENPEYLTPQG
                                                                                                                                                                                                                                           GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  494 GAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 546
                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1259 AA.
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InterPro; IPR000719; Prot_kinase.
InterPro; IPR001290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
InterPro; IPR004019; Yip_motif.
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PRODOM; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYRKC; 1.
PROSITE; PS00018; EF_HAND; 1.
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Pfam; PF01030; Recep L domain; 2.
Pfam; PF02757; YLP; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel, 22, 01-OCT-2002 (TrEMBLrel, 22, 01-OCT-2003 (TrEMBLrel, 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neu protooncoprotein.
Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 PANASLSFLQDIQEVQGYVLIAHSQVRQIPLQRLRIVRGTQLFEDNYALAVLDNGDPLEG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TINRESACPPCSPACKDAHCWGASSGDCQSLIRTVCAGGCARCKGPQPTDCCHEQCAAGCT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDVGS-----329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    546 LQGLPREYVKDRYCLPCHSECQPQNGSVTCFGSEADQCVACAHYKDPPFCVARCPSGVKP 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  786 GICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLNWCVQIAKGMSYLEDVRLVHRDL 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTNASLSFLODIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 TTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLID 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCT 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 GCKKIFGSLAFLPESFDGDPASNTAPLQPEQLRVFEALEEITGYLYISAWPDSLPNLSVF 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 FRNPHQALLHSANRPEEECVGEGLACYPCAHGHCWGPGPTQCVNCSQFLRGQECVEECRV 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            606 DLSFMPIWKFADEEGTCQPCPINCTHSCADLDEKGCPAEQRASPVTSIIAAVVGILLAVV 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       726 GSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLL 785
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                                                                                                                                                                                                                                                                                                                                                               25 WLDRSVLAKELARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYL
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                    Length 1259;
                                                                                                                                                                                                                                                                                                                44; Indels 731;
                                                                                          PROSITE; PS00018; EF HAND; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Kinase; Transferase; Tyrosine-protein Kinase.
SEQUENCE 1259 AA; 137989 MW; E37364D49C4ACD46 CRC64;
                                                                                                                                                                                                                                                               56.8%; Score 2124.5; DB 6; ilarity 36.7%; Pred. No. 5.7e-150; Conservative 18; Mismatches 44;
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    PR00109; TYRKINASE.
PD000001; Prot_kinase; 1.
                             ProDom; PD000001; Prot_Kii
SMART; SM00261; FU; 3.
SMART; SM00219; TYrKc; 1.
                                                                                                                                                                                                                                                                                          Similarity
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Mon Sep 13 07:41:03 2004

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OM protein - protein search, using sw model

September 9, 2004, 12:20:54; Search time 12.6656 Seconds (without alignments) 2836.691 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-821-883-2 3739 1 MRAAPLJLARAASLSLGFLF.......BPVQEGAPPPPAAAHHHHH 690

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P04626 homo sapien	rattr		gallı	рошо	homo	Q01279 mus musculu	rattr	homo	homo	rattu					BnB	bos t	canis	062757 felis silve		Q60481 cavia porce		_		-				_	lymn	-	rattu	P14616 homo sapien
SUMMARIES	Ω	ERB2 HUMAN		ERB2 MESAU		EGFR HUMAN	ERB4 HUMAN	EGFR_MOUSE	ERB4_RAT		CSF2_HUMAN	ERB3_RAT	XMRK XIPMA	CSF2 SHEEP	EGFR_DROME	CSF2_CEREL		CSF2_BOVIN	CSF2 CANFA	CSF2_FELCA		CSF2 CAVPO	LT23 CAEEL	CSF2_MOUSE	ILPR_BRALA	ERB2_MOUSE	HTK7 HYDAT	INSR_DROME	INSR_HUMAN	INSR_MOUSE	MIPR_LYMST	IRR_MOUSE	INSE_RAT	IRR_HUMAN
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	Query Match	64.3	52.1	51.8	20.5	19.3	19.3	19.2	19.2	18.6	18.0	17.9	17.5	14.7	14.3	14.1	13.1	12.9	12.7	12.1	11.8	11.6	10.8	•					6.9				٠.	9.9
		2405.5	1947.5	1935	755.5	721	721	717.5	717	697	674	699	655.5	549	536	529	488	481.5	476.5	452	441	435.5	404.5	367	317.5	293	273.5	270.5	256.5	252.5	252	•	249	248.5
	Result No.	-	7	m	4	2	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P14617 cavia porce P08069 homo sapien	P24062 rattus norv Q60751 mus musculu Q64716 rattus norv	Q93105 aedes aegyp Q9umn6 homo sapien	P15309 homo aapien P23246 homo aapien	O14686 homo sapien P81122 mus musculu	Q14162 homo sapien
IRR CAVPO IG1R HUMAN	IG1R_RAT IG1R_MOUSE IRR_RAT	INSE AEDAE MLL4 HUMAN	PPAP HUMAN SFPQ HUMAN	MLL2_HUMAN IRS2_MOUSE	SREC_HUMAN
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246.5	235.5 233.5 228.5	207	168 166	166 162	160
34 35	36 37 38	9 0 4	41	443	45

### ALIGNMENTS

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                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          TAS.
                                                                                                                                                                                                                                                                                                      (Potential). Interacts with PRKCABP (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
FTM: Ligand-binding increases phosphorylation on tyrosine
residues (By similarity).
POLYMORPHISM: There are fours alleles due to the variations in
positions 654 and 655. Allele B1 (Ile-654/Ile-655) has a frequency
of 0.782; allele B2 (Ile-654/Val-655) has a frequency of 0.206;
allele B3 (Val-655) has a frequency of 0.206;
SIMILARITY: Belongs to the EGF receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
EXTRACELLULAR (POTENTIAL).
alpha and amphiregulin.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                tyrosine phosphate.
SUBUNIT: Heterodimer with each of the other ERBB receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
CYTOPLASMIC (POTENTIAL)
PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                                                       EMBL, M11761, AAA35808.1; JOINED. EMBL, M11762, AAA35808.1; JOINED. EMBL, M11762, AAA35808.1; JOINED. EMBL, M11763, AAA35808.1; JOINED. EMBL, M11764, AAA35808.1; JOINED. EMBL, M11765, AAA35808.1; JOINED. EMBL, M17765, AAA35808.1; JOINED. EMBL, M1230, AAA35808.1; -.. EMBL, AY208911; AAA75493.1; -.. EMBL, X03363; CAAA7640.1; -.. EMBL, X03363; CAAA760.1; -.. EMBL, X03363; CAAA760.1; -.. EMBL, X03363; CAAA7060.1; -.. EMBL, X03363; CAAA7060.1; -.. EMBL, X03363; CAAA7060.1; -.. FDB; 1082; 18-FEB-03. FDB; 1082; 18-FEB-03.
                                                                                                                                                                                   EMBL; M11767; AAA35808.1; -.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B3; dbSNP:1801201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR 016317.
I -> V (in allele B3; dbSNP:1801201
/FTId=VAR 004077.
I -> V (in allele B2 and allele B3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2405.5; DB 1; Length 1255;
Pred. No. 9.6e-128;
0; Mismatches 3; Indels 727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VAR 016318.
MW; 39E9DFDA04DCF962 CRC64;
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   SIMILARITY)
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ATP (BY SIMILARITY
BY SIMILARITY
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Matches 509; Conservative
   1170
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5.1.6 Compugen Ltd GenCore version (c) 1993 - 2004 Copyright

OM protein - protein search, using sw model

9, 2004, 12:29:10 September Run on:

0 ; Search time 22.0271 Seconds (without alignments) 3013.200 Million cell updates/sec

Title: Perfect score:

Sequence:

US-09-821-883-2 3739 1 MRAAPLLLARAASLSLGFLF.......EPVQEGAPPPPAAAHHHHH 690

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
: pir3:\* .. ..

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	protein-tyrosine k	protein-tyrosine k	p-185 precursor -	epidermal growth f					epidermal growth f	kinase-related tra		epidermal growth f	protein-tyrosine k	granulocyte-macrop	granulocyte-macrop	epidermal growth f	granulocyte-macrop	granulocyte-macrop	granulocyte-macrop	protein let-23 [im	protein-tyrosine k	protein-tyrosine k	epidermal growth f	-	epidermal growth f			epidermal growth f	-11
SUMMARIES	QI	A24571	TVRTNU	148161	TVCHLV	A42032	GOHUE	A47253	A53183	A36325	A36223	FOHUGM	JC4387	S06142	JH0469	A61632	A27131	FOBOGM	A44936	146269	E88257	870712	S70713	GOFFE	POMSGM	D45558	A45558	B45558	D.	T43220
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	Length	1255	1260	1254	1223	527	1210	1308	1210	644	1342	144	1339	1166	144	144	843	143	144	127	1323	1374	1369	1330	153	366	1717	333	342	1363
•	Ouery Match		52.2		20.2			19.3	19.2	19.1	18.6	18.0	17.7	17.5	4	14.6	14.3	12.9	12.7	11.8	10.8	10.8	10.4	•	10.0		9.1			8.5
	Score	2405.5	1950.5	1935	755.5	754.5	721	721	717.5	714.5	697	674	662	655.5	549	545	536	481.5	476.5	441	404.5	404.5	390.5	375.5	374	341	341	331	331	317.5
	Result No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

protein-tyrosine k insulin receptor (	insulin receptor - insulin receptor p insulin receptor p	insulin-like growt insulin receptor p	insulin-like growt insulin-like growt insulin receptor-r	tyrosine kinase re insulin-like growt insulin receptor-r	ingulin-like growt ingulin receptor - ingulin receptor h
T18534 S57245	AS6081 INHUR A34157	T43212 A36080	A36502 IGHUR1 B47417	JH0803 A33837 B36502	A48805 T30346 T42047
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273.5	270.5 256.5 252.5	252 249	246 246 238	235.5 235.5 231.5	223.5 207 188
30	3 3 3 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	36 2	38 30 30 30	4 4 4 2 1 2	4 4 4 6 4 6

### ALIGNMENTS

KESULI 1
A24571
protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human
N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbE
C. Caronica. Home annione (man)

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence revision 06-Dec-1996 #text\_change 11-Jun-1999
C;Accession: A24571; A25491; A44188; B44188; I59509; I57622
R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.;
R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.;
A;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.;
A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth f
A;Reference number: A24571; MUID:86118663; PMID:3003577

A; Accession: A2457]

A; Molecule type: mRNA
A; Residues: 1-1255 < YAM>
A; Residues: 1-1255 < YAM>
A; Residues: 1-1255 < YAM>
A; Cross-references: GB: X03363; NID: g31197; PIDN: CAA27060.1; PID: g31198
A; Cross-references: GB: X03363; NID: g497-6501, 1985
Broc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
A; Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epiderm
A; Reference number: A25491; MUID: 86016729; PMID: 2995967

A;Accession: A25491
A;Molecule type: DNA
A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
B;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
B;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
B;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromos
A;Reference number: A44188; MUID:86070181; PMID:2999974

A;Molecule type: DNA X;Residues: 740-910 <COUI> A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A;Accession: B44188

A;Molecule type: mRNA
A;Residues: 1-517, 'RALL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <COU2>
A;Residues: 1-517, 'RALL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <COU2>
A;Cross-references: GB:M11730; NID:g183986
R;King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A;Reference number: 159509; MUID:85272597; PMID:2992089
A;Accession: 159509

A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:L29395; NID:9459807; PIDN:AAA35809.1; PID:9459808
B;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
R;Tal, M.; King, C.R.; Promocre: evidence for multiple mechanisms for transcriptional
A;Title: Human HER2 (neu)
A;Reference number: 157622; MUID:87286898; PMID:3039351

A;Accession: I57622 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-191 <TAL>

A; Cross.	references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332	qq	616 FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVLGVVFGILI 675
C, Genet:		ò	330 329
A, Gene: A, Cross	GDB:ERBB2; NGL; NEU; HEK-2 -references: GDB:120613; OMIM:164870	qq	676 KRRQQKIRKYTWRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 735
A; Map po	Saltion: 1742.1-17421.1 18: 25/1; 75/3: 14/1; 883/3	λō	330 329
C; Funct:		තු	736 KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDBAYVMAGVGSPYVSRLLGICLTSTVQ 795
A; Descr C; Super1	Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by Air Superfamily: epidermal growth factor receptor; protein kinase homology	ò	330 329
inase	cas: AIF; aucopnosphorylation; auplication; glycoprotein; phosphoprotein; phospho	qq	796 LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS 855
F; 22-125	Domain: Signal Sequence #Status predicted <slg> SS/Croduct: protein-tyrosime kinase erb82 #status predicted <mat></mat></slg>	λ	330 329
F; 70-304	<pre>// Johnain: GXTraceliular #status predicted &lt; EXI'&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain repeat &lt; EBI&gt; // Domain: EGF receptor extracellular domain receptor extrace</pre>	ą a	856 PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 915
F;654-6	2	à	330 329
F;718-98	253/ Domain: Intracellula #Bucue predicted vinis 33/Domain: protein kinase homology KINs	đ	916 MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE 975
F; 68, 124	34, Region: Protein Kinase Alf-Dinding Moti. 4,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predict	ò	330 329
F;753/Ac	#scacae	ପ୍ର	976 FSRWARDPQRFVVIQNEDLGFASPLDSTFYRSLLEDDDWGDLVDABEYLVPQQGFFCPDP 1035
Query Best I	Match 64.3%; Score 2405.5; DB 1; Length 1255; Local Similarity 41.1%; Pred. No. 1.4e-125;	දු අ	330GAGGWVHHRHRSSSTRSGGGDLTLGLEPSEERAPRSPLAPSEGAGSDVFDGDLGMGAA 387 
Matches	509; Conservative (	Š	388 KGLOSLPTHDPSPLORXSEDPTVPLPSETDGYVAPLTCSPOPEYVNOPDVRPOPPSPREG 447
के ह	35 LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ 94	qq	KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG
ò	-	oy Op	448 PLPAARPAGATLIBRAKTLSPGKNGVVKDVFAFGGAVENBEYLTPQGGAAPDPHPPPAFSP 507 
QQ	76 DIÓEVQGYVLIAHNOVRQVPLORLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 135	Š	508 AFDNLYYWDODPPERGAPPSTFKGTPTAENPEYLGLDVP 546
کن م	155 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC 214	3 da	1216 AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 1254
ò	215 SPMCKGSRCWGBSSEDCQSLTRIVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC 274	RESULT 2 TVRTNU	
Db	196 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC 255	protein-t	yrosine kinase (BC 2.7.1.112) neu precursor - rat : Rattus norvedicus (Norway rat)
å í	LHFNHSGICELHCPALVTYNTDTPESMPNDEGRYTFGASCVTACPYNYLSTDVGS 329	C;Date: 3 C;Accessi	C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999 C;Accession: A24562; A61204
a 8	256 LHFNHSGICELHCPALVTYNIDTFESMFNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC 315	K;Bargman Nature 31 A:Title:	In C.11.; Hung, M.C.; Welnberg, K.A. 19, 226-230, 1986 The new oncodene encodes an epidermal growth factor receptor-related protein.
S 8	PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 375	A; Referen	ce number: A24562; MUID:86118662; PMID:3945311 on: A24562
ò	330 329	A;Molecul A;Residue	e type: mkNA is: 1-1260 <bar></bar>
Db	376 FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI 435	A;Cross-r R;Masui,	rereronces: EMBL:X03382; NIL:gob/45; FILN:CAAZ/USY.1; FIL:gob/40 A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen,
ò	330 329	A;Title:	Thesis 12, 1973-1978, 1991 Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no my sequencing of the rating of the ration of the ra
QQ	436 LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 495	A;Referen	<pre>// 11.02mmmade O1 N-metaly1-N-mitalOcourea. ce number A61204; MUID:92035293; PMID:1682063</pre>
È	330 329	A;Status:	or: preliminary present nul
Dp	496 TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV 555	A;Residue	is: CIPC. CAN. VV, 665-702 <mas> uthors translated the codon GCA for residue 25 as Val</mas>
ò	330 329	C, Genetic	8:
qq	556 NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615	C; Superfa	ica. mily: epidermal growth factor receptor; protein kinase homology m: ATD: antophorphorylation: dumlication: glycoprofein: phosphoprotein: phospho
ò	330 329	F;1-19/Do F;20-1260	main: signal sequence #status predicted <sig> //Product: protein-tyrosine kinase neu #status predicted <mat></mat></sig>



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September 9, 2004, 12:41:37 ; Search time 72.9649 Seconds (without alignments) 3032.635 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 2, Appli	Sequence 4, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 6, Appli	Sequence 9, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 126, App	Sequence 6, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 28, Appl	Sequence 594, App
ID	US-09-821-883-2	US-09-821-883-4	US-09-821-883-1	US-09-821-883-3	US-09-854-356-6	US-09-811-123-9	US-09-811-115-3	US-09-769-508-2	US-09-984-092-4	US-10-177-293-126	US-10-207-498-6	US-10-338-730-2	US-10-322-892-4	US-10-272-437A-28	US-10-117-937-594
DB	6	0	σ	σ	Q	σ	0	Q	12	14	14	14	14	15	15
* Query Match Length DB	069	697	555	564	919	1255	1255	1255	1255	1255	1255	1255	1255	1255	1255
% Query Match	100.0	92.9	79.5	79.1	68.8	64.5	64.5	64.5	64.5	64.5	64.5	64.5	64.5	64.5	64.5
Score	3739	3473.5	2972	2957.5	2573.5	2410.5	2410.5	2410.5	2410.5	2410.5	2410.5	2410.5	2410.5	2410.5	2410.5
Result No.		7	e	4	5	9	7	60	6	10	11	12	13	14	15

Sequence 36, Appl Sequence 4, Appli Sequence 126, App Sequence 1, Appli Sequence 2, Appli	Sequence 6, Appli Sequence 3, Appli Sequence 553, App Sequence 2, Appli Sequence 3, Appli	Sequence 45, Appl Sequence 2, Appli Sequence 17, Appl Sequence 553, App Sequence 661, Appl Sequence 68, Appl		Sequence 2, Appli Sequence 1, Appli Sequence 13, Appl Sequence 3, Appli Sequence 4, Appli Sequence 11, Appli Sequence 17, Appli
15 US-10-435-696-36 16 US-10-441-779C-4 16 US-10-734-564-126 9 US-09-854-356-1 9 US-09-930-125-2	10 US-09-441-411-6 12 US-10-469-162-3 12 US-10-253-286-553 12 US-09-765-973-2 12 US-10-418-027-3	14 US-10-207-655-45 14 US-10-313-644-2 15 US-10-394-322A-17 15 US-10-245-871-553 15 US-10-149-138-4641 16 US-10-647-005-68	16 US-10-149-138-4641 14 US-10-146-473-72 9 US-09-812-881-5 9 US-09-854-356-14 9 US-09-870-759-118 10 US-09-751-708A-118	9 US-09-854-356-2 9 US-09-921-161-1 14 US-10-268-501-13 15 US-10-608-626-13 9 US-09-854-356-3 15 US-10-412-804A-4 15 US-10-412-804A-11 9 US-09-854-356-7
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2410.5 2410.5 2410.5 2405.5 2405.5	2405.5 2405.5 2405.5 2405.5 2405.5	2405 2405 2405 2405 2405 35 35 35 35 35 35 35 35 35 35 35 35 35	2405.5 2398.5 2188.5 1961 1950.5	1948 1612 1612 1612 1612 1612 1612
16 17 18 19	22 23 24 25 25	26 28 30 30 31	3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	8 6 6 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6

### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQL 180
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                                                                                 APPLICANT: Laus, Rether
APPLICANT: Laus, Rether
APPLICANT: Uidovic, Damir
APPLICANT: Garddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFRENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US 60/193, S04
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEATURE:
; OTHER INFORMATION: HER500-hGM-CSF construct
US-09-821-883-2
              Sequence 2, Application US/09821883
Patent No. US20020061310Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2
LENGTH: 690
US-09-821-883-2
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361 TLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP
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Sequence 1, Application US/09821883;

Patent No. US20020063310A1

GENERAL INFORMATION:

APPLICANT: Laus, Reiner

APPLICANT: Graddis, Thomas

TITLE OF INVENTION: Compositions and Methods for Dendritic

TITLE OF INVENTION: Coll-Based Immunotherapy

FILE OF INVENTION: Coll-Based Immunotherapy

FILE REFERENCE: 756-0022.30

CURRENT APPLICATION NUMBER: US/09/821,883

CURRENT FILING DATE: 2000-03-30

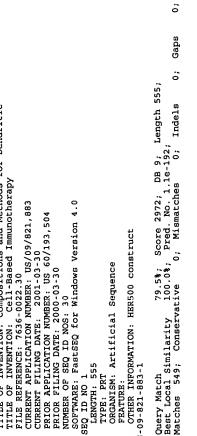
NUMBER OF SEQ ID NOS: 30

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENTING DATE: 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: HER500 construct US-09-821-883-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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US-09-821-883-1
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91.7%; Pred. No. 1.7e-226;
ive 19; Mismatches 28; Indels 11;
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Sequence 4, Application US/09821883
Patent No. US20020061310A1
GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Udovic, Damir
APPLICANT: Graddis, Thomas
ITILE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REPERENCE: 766-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 697
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Best Local Similarity 91.77
Matches 641; Conservative
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GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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Sequence 10, Appl Sequence 4, Appl1 Sequence 7, Appl1 Sequence 2, Appl1 Sequence 2, Appl1 Sequence 2, Appl1 Sequence 4, Appl1 Sequence 4, Appl1 Sequence 4, Appl1 Sequence 14, Appl Sequence 144, Appl Sequ		Length 1255; Indels 727; Gaps 1; QGNLELTYLPTNASLSFLQ 94	/LDNGDPLNNTTPVTGASPG 154	NQLALILIDINRSRACHPC 214	CHEQCAAGCTGPKHSDCLAC 274	CUTACPYNYLSTDVGS 329	329	TSANIQEFAGCKKIFGSLA 375
US-08-484-438-10 US-08-484-438-4 US-08-484-438-7 US-08-484-438-7 US-08-484-438-2 US-09-570-454-2 US-09-570-454-2 US-09-570-454-2 US-09-570-454-2 US-09-570-454-2 US-08-438-9 US-08-475-352-4 US-08-475-352-4 US-08-475-352-4 US-08-468-6094-144 US-08-468-6094-144 US-08-468-6094-144 US-08-468-6094-144 US-08-762-227A-144 US-08-762-227A-144 US-08-762-227A-144 US-08-762-227A-144 US-08-762-227A-144 US-08-762-227A-144 US-08-762-227A-144	9527487 186601C PEPTIDES 105/09/527,487	64.5%; Score 2410.5; DB 4; Length 1255; imilarity 41.2%; Pred. No. 3.7e-179; ); Conservative 0; Mismatches 2; Indels 727; GallargasTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLS:	DI GEVOGYVLI AHNOVRQVPLORLRI VRGTQLPEDNYALAVLDNGDPLNNTTPVTGASPG 	GLRELOLRSLTEILKGGVLIORNPQLCYODTILWKDIFHKNNQLALTLIDTNRSRACHPC 	EDCOSLIRIVCAGGCARCKGPLPTDCCHB                   EDCOSLIRIVCAGGCARCKGPLPTDCCHB	SMPNPEGRYTFGAS 		PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKI FGSLA
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28 30 31 31 31 32 34 34 36 36 69 69 40 69 41 69 69 69 69 69 69 69 69 69 69 69 69 69	RESULT 1 US-09-527-487-2 Sequence 2, Applicatio Patent No. 6238060 GENERAL INFORMATION: APPLICANT: Nicolette, TITLE OF INVENTION: FILE REFERRICE: 12689 CURRENT APPLICATION NY CURRENT FILING DATE: NUMBER OF SEQ ID NOS: SOFTWARE: Patent IN Ve TENGTH: 1255 TENGTH: 1255 TENGTH: 1255 US-09-527-487-2	Query Match Best Local Si Matches 510; Qy 35 L Db 16 L	Qy 95 I	Qy 155 q	Qy 215 g	Oy 275 I	Oy 330 -	Db 316 F

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436 LHNGAYSLTLQGLGISWLGLRSLRBLGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 495	; TYPE: PRT ; ORGANISM:	PRT ISM: Homo sapiens
330 329	US-09-811-115	اع
496 TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV 555	Query Match Best Local S	64.5%; Score 2410.5; DB 4; Length 1255; imilarity 41.2%; Pred. No. 3.7e-179;
330 329	Matches	; Conservative 0; Mismatches 2; Indels 727; Gaps
556 NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615	ò	35 LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ 94
330 329	අු	16 LPPGAASTQVCTGTDMKLRLPASPRTHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ 75
616 FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILI 675	ò	95 DIQEVQCYVLIAHNQVRQVPLQRIRIVRGTQLFEDNYALAVLDNGDPLANTTPVTGASPG 154
330 329	qu	76 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 135
676 KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 735	'n	155 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLALTLIDTNRSRACHPC 214
330 329	q	136 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC 195
736 KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ 795	ò	215 SPWCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLFTDCCHEQCAAGCTGPKHSDCLAC 274
330 329	ପ୍	196 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPRHSDCLAC 255
796 LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS 855	ò	275 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 329
330 329	ପ	256 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC 315
856 PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 915	ò	330 329
330 329	අය	316 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 375
916 MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE 975	ò	330 329
330 329	q	376 FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLXISAWPDSLPDLSVFQNLQVIRGRI 435
976 FSRMARDPQREVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDABEYLVPQQGFFCPDP 1035	ò	330 329
330GAGGWVHHRHRSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA 387	qa	436 LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 495
1036 APGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA 1095	ò	330 329
388 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG 447	qa	496 TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV 555
1096 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG 1155	ò	330 329
448 PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP 507	đũ	556 NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615
1156 PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP 1215	'n	330 329
508 APDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 546	qa	616 FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILI 675
1216 AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 1254	ò	330 329
	qu	676 KRRQQKIRKYTWRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 735
1-115-3	ò	330 329
; Sequence 5, Application 05/03011115 ; Patent No. 6612979	qq	736 KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ 795
APPLICANT: Bricken, Sharon	λ'n	330 329
double statement store or a	đ	796 LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS 855
OF INVENTION: HER-Z TRANSGENIC NON-HUMAN TUMOR MODEL REFERENCE: GENENT.034A	ò	330 329
CURRENT APPLICATION NUMBER: US/09/811,115 CURRENT FILING DATE: 2001-03-16	qa	856 PNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESILRRRFTHQSDVWSYGVTVWEL 915
APPLICATION NUMBER: 60/189,844 FILLING DATE: 2000-03-16	ò	330 329
NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0	<u>අ</u>	916 MIFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE 975

5.1.6 Compugen Ltd. GenCore version (c) 1993 - 2004 Copyright

- protein search, using sw model OM protein 9, 2004, 12:20:15; Search time 75.9936 Seconds (without alignments) 2565.449 Million cell updates/sec September Run on:

US-09-821-883-2 Title: Perfect score:

1 MRAAPLLLARAASLSLGFLF.......EPVQEGAPPPPAAAHHHHH 690 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB M

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\*

11: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

5: geneseqp2001s:\*

5: geneseqp2003s:\*

7: geneseqp2033s:\* geneseqp2004s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

1	HER	HER	HER	HER	HER	/nen	her	tran	tyr	HER		HER	t Ca	Her	G-6	erb	Erb	epi	/nen	HER	aci	HER	nen		Her
	Human	Human	Human	Human	Human	Her-2,	Human		Human	Human	Human	Human	Breas	Human	Human	Human	Human	Human	HER-2,	Human	Amino	Human	HER2/1	Human	Human
	Aae13109	Aae13111	Aae13108	Aae13110	4ab21203	Aam51148	4ay92620	4ab60167	Aae12130	Aae26349	4ae26366	4au74545	Abr47447	4bp74708	Aae38390	Ada38143	4da37255	4db67621	Aaw01111	Aaw92406	Aay84780	Aab21198	Aag88267	Aab85458	Aae20479
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	AAE13109	AAE13111	AAE13108	AAE13110	AAB21203	AAM51148	AAY92620	AAB60167	AAE12130	AAE26349	AAE26366	AAU74545	ABR47447	ABP74708	AAE38390	ADA38143	ADA37255	ADB67621	AAW01111	AAW92406	AAY84780	AAB21198	AAG88267	AAB85458	AAE20479
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AAU77114	AAM51143	AAE24067	ABR43687	ABR82066	ADC09593	ADD25484	ADE63281	ADE76190	AAR39568	ADC35106	AAU98923	AAW19764	AAE13112	AAM51153	AAM51152	AAB21208	AAB21206	AAG62860	AAM51151
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2405.5	2405.5	2405.5	2405.5	2405.5	2405.5	2405.5	2405.5	2405.5	2400.5	2398.5	2334.5	2224	2188.5	2130	2129	2092.5	1961	1961	1961
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

Immunostimulatory fusion protein; IFP; antigen component; therapy; immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; PAP protein; Ala Arg linker; membrane distal extracellular domain; C-terminal tag; human; GM-CSP; HER-2 protein; granulocyte-macrophage colony stimulating factor; Human HER500-hGM-CSF fusion protein construct. AAE13109 standard; protein; 690 AA 28-JAN-2002 (first entry) AAE13109; 

WO200174855-A2 Homo sapiens. Synthetic. Chimeric.

30-MAR-2001; 2001WO-US010515.

11-OCT-2001.

(DEND-) DENDREON CORP

30-MAR-2000; 2000US-0193504P.

Laus R, Vidovic D,

Graddie T;

WPI; 2001-662965/76. N-PSDB; AAD21565.

An immunostimulatory fusion protein comprising the intracellular domain of HER-2 and an antigen elicits an immune response to the antigen and is useful for the treatment of associated cancer associated.

Claim 7; Page 26; 59pp; English.

The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IPPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular

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immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 hGM-CSF fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular and intracellular domains, an Ala Ala linker, a mature human granulocyte- macrophage colony stimulating factor (GM-CSF) sequence and a C-terminal tag
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Human HER500-rGM-CSF fusion construct comprising OVA-derived peptide.
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                                       AAE13111 standard; protein; 697
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                                                                                                                    28-JAN-2002
                                                                               AAE13111;
RESULT 2
AAE13111
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SXSXSXB

240

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The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC) induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 rGM-CSF fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular domain, an Ala linker, an ovalbumin (OVA)-derived immunodominant cotapeptide, HER-2 granulocyte-macrophage colony stimulating factor (GM-CSF) sequence and a
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                                immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; pAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; GM-CSF; HER-2 protein; granulocyte-macrophage colon; stimulating factor; ovalbumin-derived octapeptide; OVA; rat; HER500-rGM-CSF fusion protein.
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                 component; therapy;
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91.7%; Pred. No. 2.4e-207;
ive 19; Mismatches 28;
                   Immunostimulatory fusion protein; IFP; antigen
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using frame plus p2n model
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September 10, 2004, 05:57:41; Search time 3742.37 Seconds (without alignments) 4428.608 Million cell updates/sec Run on:

US-09-821-883-1 Title: Perfect score:

1 MRAAPLLLARAASLSLGFLF.....BNPEYLGLDVPAAAHHHHH 555 Sequence:

**BLOSUM62** Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

27513289 segs, 14931090276 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
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-MODBL=frame+ p2n.model -DEV=xlh
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-UNITS=bits -START=1 -END=-1 -MATRIX=000-TRR MIN=0\_-ALIGN=15 -MODE=LOCAL
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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### ALIGNMENTS

AK031099 LOCUS DEFINITION RESULT 1

AK031099

Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930404NNO product:v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived AK031099

AK031099.

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

VERSION KEYWORDS SOURCE ORGANISM ACCESSION

us-09-821-883-1.rst

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B dachi,J., Alzawa,K., Hara,A., Hashizume,W.,

Rydads,S., Furuno,M., Hangaki,T., Hara,A., Hashizume,W.,

Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,

Rydashida,K., Mayatsu,N., Militana,Y., Kondo,H., Kouda,M.,

Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,

Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,

Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,

Okazaki,Y., Saito,R., Satoh,H., Sakai,C., Sakai,K., Sakazume,N.,

Sano,H., Saeaki,D., Shibata,K., Shinagawa,A., Shizaki,T.,

Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,

Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Submitted (16-Jul-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

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Kanagawa 230-0045, Japan (E-mail:genome-reseasc.riken.go.jp,

URL:http://genome.gec.riken.go.jp/, Tel:81-45-503-9222,

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                                                                                                                                                                                                                          Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Nature 409, 685-690 (2001)
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                      Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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/organism="Mus musculus" /mol\_type="mRNA" /strain="C57BL/63"

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FEATURES

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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Sequence 15, Appl Sequence 11, Appl Sequence 125, Appl Sequence 119, App Sequence 1, Appli Sequence 124, Appli Sequence 121, Appli

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Sequence 6, Application US/09821883
; Patent No. US2002061310A1
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Jaus, Reiner
; APPLICANT: Jaus, Reiner
; APPLICANT: Original Thomas
; TITLE OF INVENTION: Compositions and Methods for Dendritic
; TITLE OF INVENTION: Cell-Based Immunotherapy
; FILE REFERENCE: 7636-0022.30
; CURRENT APPLICATION NUMBER: US/09/821,883
; CURRENT APPLICATION NUMBER: US 60/193,504
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1665
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        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Facent No. US2020061310A1
GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
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Sequence 1 Sequence 1 Sequence 5 Sequence 1 Sequence 1 Sequence 4

Perfect score:

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Scoring table:

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Sequence 9, Application US/08229515A
Fatent No. 5518885
GENERAL INCRNATION:
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: REBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
CONTRESS: GEOSTGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: usa
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIFTCATION + 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELEFAX: 404-688-0770
TELEFAX: 404-688-0700;
TELEFAX: 404-688-0700;
TELEFAX: 404-688-0700;
TELEFAX: 404-688-0770
TELEFAX: 404-688-0860
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  STATE: Georgia
COUNTRY: usa
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-MODEL-frame+ p2n.model -DEV=xlh
-MODEL-frame+ p2n.model -DEV=xlh
-DB=189u6d PatenTe NA -QFWT=fastep -SUFFIX=rni -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=51te -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-USRB=LOSALIGN=200 -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPELOCK=10 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -TRREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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11. /GgTa_6/ptodatea/2/ina/5A_COMB.seq:*
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33. /GgTa_6/ptodatea/2/ina/6A_COMB.seq:*
43. /GgTa_6/ptodatea/2/ina/6B_COMB.seq:*
45. /GgTa_6/ptodatea/2/ina/PCTUS_COMB.seq:*
55. /GgTa_6/ptodatea/2/ina/PCTUS_COMB.seq:*
66. /GgTa_6/ptodatea/2/ina/Patea/1.seq:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-229-5	15A-9	. ଶ	TITGAGICCATGCCCAAICCCGAGGGCCGGTATACATITGGCGCCCAGGTGTGAGTGACTGCC
Alignment Scores Pred. No.: Score: Percent Similari	1.67e-178 Length: 2416.00 Matches: 5 y: 41.14% Conservative: 5	ζς Op	318 CysProTyrAsnTyrLeuSerThrAspValGlySer
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		ପ୍ର	CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGGCCAG
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	AsnHisSerGlvIleCvsGluLeuHisCvsProAlaLeuValThrTvrAsnThrAsoThr	δ	
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(c) 1993 - 2004 Compugen Ltd
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                                                                                                                                                                                                                           The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. The prescrivated dendritic cells are used to treat cancer egs breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 fusion DNA construct which comprises DNA molecules encoding human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular and intracellular domains and a C-terminal tag
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                                                                                                                                                CysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAspAsnGlnLeuAlaLeu
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                                                                                                                                                                                                                                                                                                                                                                                                ATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCCAGCTGTGTGACTGCCTGTCCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnTyrLeuSerThrAspValGlySerGlyAlaGlyGlyMetValHisHisArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerSerSerThrArgSerGlyGlyGlyAspLeuThrLeuGlybeuGluProSerGluGlu
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                                                                      LeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGlnLeu
                                                                                             CTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAGCTC
                                                                                                                                                                  ThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLysGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGlnArgTyrSerGluAapProThrValProLeuProSerGluThrAspGlyTyrVal
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                     SUMMARIES
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BD267515
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AX587649
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Cgn2_1/USFVO_smodel -DEV=xlh
-Q=/Cgn2_1/USFVO_smodel -DEV=xlh
-Q=/Cgn2_1/USFVO_smodel -DEV=xlh
-Q=/Cgn2_1/USFVO_smodel -USFX=xee -MINNATCH=0.1 -LOOFCL=0 -LOOPEXT=0
-UNITS=b1te -GTPAT=1 -END=-1 -MATRIX=100 -TRANS=human40.cdi -LIST=45
-UNITS=b1te -GTPAT=1 -END=-1 -MATRIX=100 -TRANS=human40.cdi -LIST=45
-UNITS=b1te -GTPAT=1 -END=-1 -MATRIX=100 -TRANS=human40.cdi -LIST=45
-UNITS=bte -GTPAT=1 -END=-1 -MATRIX=000000000
-UNITS=bte -ONDH=ext -HEAPSIZE=50 -MINLEN=-0 -MAXLEN=2000000000
-UNER=US09821883 @CGN 1 1 16795 @runat 09092004 105127 6631 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUER* -NGE GCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-FGAPON=10 -WARN -LISTOUT=30 -TRIREDUT=30 -TRIREDUT=12 -XGAPON=10 -XGAPON=6
-FGAPON=17 -YGAPON=10 -YGAPON=0.5 -FGAPON=6
                                                                1; Search time 5945.99 Seconds (without alignments) 4045.651 Million cell updates/sec
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1 MRAAPLLLARAASLSLGFLF.......ENPEYLGLDVPAAHHHHH 555
                                                                                                                                                                                                                                           6940544
   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                             - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                     3470272 seqs, 21671516995 residues
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                  September 10, 2004, 05:41:11
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                               Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
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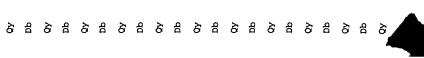
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121124 Sequence 9
159745 Sequence 9
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AR202597 Sequence AX344811 Sequence AX587649 Sequence AX744071 Sequence BD005474 Cellular MIN130 Human Lyros AX714070 Sequence AX060703 Sequence AX180403 Sequence AX181438 Sequence AX467229 Sequence AX360741 Sequence AX46726 Sequence AX36094 Sequence AX360

AX268285 Sequence AX268287 Seguence AX268286 Seguence AX268288 Sequence

ALIGNMENTS

			1201 CTACAGCGGTACAGTGAGGACCCCACAGTACCCCTGCCCTCTGAGACTGATGGCTACGTT 12   1201 CTACAGCGGTACAGTGACCCCACAGTACCCCTGCCCTCTGAGACTGATGGCTACGTT 12   421 AlaProleuThrCysSerProGlnProGluTyrValAsnGlnProAspValArgProGln 44   1261 GCCCCCTGACCTGCAGCCCCAGCCTGAATATGTGAACCAGCCAG	### ### ##############################	2000	Qy         521 GluàrgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluàsnProGluTyr 540           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
AX268285  AX268285  DEFINITION  AX268285  ACCESSION  AX268285  VERSION  AX268285  VERSION  AX268285  AX268	Alignment Scores:  Pred. No.:  Pred. No.:  Score:  Sco	Qy         1 MetArgAlaAlaProLeuLeuAlaArgAlaAlaSerLeuGlyPheLeuPhe 20	Qy         41 SerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGluThr         60	Oy         81 LeuThrTyrLeuProThrAsnalaSerLeuSerPheLeuGinAspileGinGluValGin 100           Db         241 CTCACCTACCTGCCCACCAACCCTGTCCTTCCTGCAGGATTCCAGGAGGTGCAG 300           Oy         101 GlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGinArgLeuArgIle 120           Db         301 GGCTACGTGCTCATCGCTCACAACCAAGTGAGGCAGGTCCCACTGCAGAGGCTGCGGATT 360		oginteu 1         ccAGCTC 5	201 ThrLeulleaspThrasnargSerargalaCysHisProCysSerProMetCysLysGly 2



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Q9uk79 homo sapien
Q80y89 mus musculu
Q8c0e7 mus musculu
Q8r2x1 mus musculu
Q14256 homo sapien
Q8wyv0 homo sapien
Q7sy19 brachydanio
Q90836 gallus gall
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Q9wvf5 mus musculu
Q9ep98 mus musculu
Q9qx70 rattus norv
Q8mil8 sus scrofa
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Q9uk79 homo sanien
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                                                           September 9, 2004, 12:28:07; Search time 55:1456 Seconds (without alignments) 3175.456 Million cell updates/sec
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3020
1 MRAAPLLLARAASLSLGFLF.......BNPEYLGLDVPAAAHHHHH 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                1017041
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                             1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                        - protein search, using sw model
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Q8uw84 paralichthy	Q8UW84	13	1412	9.8	259.5	45
	073798	13	1358	•	263	44
T	Q9VD94	ស	2144	9.0	270.5	43
~	093457	13	1418	•	272.5	42
	QBUWB3	13	1418	9.1	273.5	41
	088459	1	89	•	273.5	40
ø	QBTOW6	ഗ	1749	•	274	39
Q9njv5 biomphalari	O9NJV5	'n	1671	•	289	38
	Q9U5A8	ហ	1472	•	291	37
	Q86MD7	Ŋ	1564		305	36
	Q9Y1X8	Ŋ	1193		323.5	35
	026568	'n	342	11.0	331	34
Q26567 schistosoma	026567	ഗ	334	11.0	331	33
Q26566 schistosoma	026566	S	1717		341	32
	Q26569	'n	366		341	31
	023821	ហ	1368		377	30
	Q9BG65	9	151		395	5
O	Q9BG64	ø	150		398	58
9	Q9W6F6	13	1137	13.5	407	27
'O	Q86NZ2	ഗ	1322		537	56
	6нін60	'n	1433	18.0	543	25
ರ	OBMLWO	Ŋ	1377	8	556	24
4 fugu r	P79754	13	1328	ö	608	23
O9psh2 gallus gall	Q9PSH2	13	599		641.5	22
	QBAWB1	13	1305	ä	657.5	21
Q9yh40 xiphophorus	Q9YH40	13	1165	ζ.	664.5	20
æ	Q9BUD7	4	331	щ.	697	19
	Q7SZF7	13	1191		703	18
Q9ese0 rattus norv	OBSE60	11	478	23.3	704.5	17

### ALIGNMENTS

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OLD OLSTAIS PRELIMINARY; PRT; 1259 AA.

AC 018735

DI 018736

DI 018737

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TRAIN-BILX;

Watson P.A., Kim K.-S., Gould M.N.;

Watson P.A., Kim K.-S., Kim K.-S., Gould M.N.;

Watson P.A., Kim K.-S., Kim K.-S., Gould M.N.;

Watson P.A., Kim K.-S., Gould M.N.;

Watson P.A., Kim K.-S., Gould M.N.;

Watson P.A., 
                                                                                                                                                                                                                                                                                                                    1026 QOGFFCPEPTPGAGGTAHRRHKSSSTRNGGGELTLGLEPSEEEPPKSPLAPSEGAGSDVF 1085
                                                                                                                                                                                                                                                                                                                                                                                                  966 PRFRELVAEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVP 1025
                                                                                                                                                                                                                                                                                            DGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVR 438
                                                                                                                                                                                                                                                                                                                                                                              PQPPSPREGPLPAARPAGATLER----AKTLSPGKNGVVKDVFAFGGAVENPEYLTPQG 493
AARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESIPPRRFTHQSDVW 905
                                                                                SYGVTVWELMTFGAKPYDG1PARE1PDLLEKGERLPQPP1CT1DVYM1MVKCWM1DSECR
                                                                                                                                                                                                            -GAGGMVHRRRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEGAGSDVF
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 GAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1259 AA.
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InterPro; IPR00219; Prot_kinase.
InterPro; IPR02290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
InterPro; IPR008266; Tyr_pkinase_AS.
InterPro; IPR004019; YrP_motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0109; TYRKINASE.
Prodom; PD000001; Prot kinase; 1.
SMART; SM00220; S_TKc; 1.
SMART; SM00219; TYRK; 1.
PROSITE; PS00018; EF_HAND; 1.
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Pfam; PF01030; Recep L domain;
Pfam; PF02757; YLP; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neu protooncoprotein.
Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TINRFSACPPCSPACKDAHCWGASSGDCQSLTRTVCAGGCARCKGPQPTDCCHEQCAAGGT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDVGS..... 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 QNLRVIRGRVLHDGAYSLTLQGLGISWLGLRSLRELGSGLALIHRNARLCFVHTVPWDQL 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     666 VGLVLGILIKRRRQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVL 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       726 GSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLL 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       786 GICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLNWCVQIAKGMSYLEDVRLVHRDL 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- 329
                                                                                                                                                                                                                                                                                                                                                                                                    PTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 TTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLID 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 TDVGSCTLVCPLNNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 GCKKIFGSLAFLPESFDGDPASNTAPLQPEQLRVFEALEEITGYLYISAWPDSLPNLSVF 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  606 DLSFMPIWKFADEEGTCQPCPINCTHSCADLDEKGCPAEQRASPVTSI1AAVVGILLAVV 665
                                                                                                                                                                                                                                                                                                                                            6 WCRWGLLLALIPSGAAGTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYL 65
                                                                                                                                                                                                                                                                                                                    25 WLDRSVLAKELARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYL
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                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                             70.3%; Score 2124.5; DB 6; Length 1259; 36.7%; Pred. No. 1.4e-153; ive 18; Mismatches 44; Indels 731;
                     ProDom; PD000001; Prot Kinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00219; TyrKc; 1.
PROSITE; PS001019; PF HAND; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SEQUENCE 1259 AA; 137989 MW; E37364D49C4ACD46 CRC64;
    PR00109; TYRKINASE.
PD000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                             460; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 9, 2004, 12:20:54; Search time 10.1875 Seconds (without alignments) 2836.691 Million cell updates/sec Run on:

US-09-821-883-1 3020 1 MRAAPLJLARAASLSLGFLF.......BNPEYLGLDVPAAAHHHHH 555 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 141681 seqs, 52070155 residues Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | P04626 homo sapien | rattu    | Q60553 mesocricetu | gallı      | homo       | homo       | พนธ ก      | Q62956 rattus norv | P21860 homo sapien | Q62799 rattus norv |            | -          |            |            | _          | Q25197 hydra atten | -          |            | _          |            | Q9wtl4 mus musculu |          | P14616 homo sapien | _         | P08069 homo sapien |          | Q60751 mus musculu | Q64716 rattus norv | Q93105 aedes aegyp | 뛶          | 1122 mus m | 3246 homo  | O14686 homo sapien |
|-----------|----------------|--------------------|----------|--------------------|------------|------------|------------|------------|--------------------|--------------------|--------------------|------------|------------|------------|------------|------------|--------------------|------------|------------|------------|------------|--------------------|----------|--------------------|-----------|--------------------|----------|--------------------|--------------------|--------------------|------------|------------|------------|--------------------|
| SUMMARIES | QI             | ERB2 HUMAN         | ERB2_RAT | ERB2 MESAU         | EGFR_CHICK | EGFR_HUMAN | ERB4_HUMAN | EGFR_MOUSE | ERB4_RAT           | ERB3 HUMAN         | ERB3 RAT           | XMRK_XIPMA | EGFR_DROME | LT23_CAEEL | ILPR BRALA | ERB2_MOUSE | HTK7_HYDAT         | INSR_DROME | INSR_HUMAN | INSR_MOUSE | MIPR_LYMST | IRR_MOUSE          | INSR_RAT | IRR_HUMAN          | IRR_CAVPO | IG1R_HUMAN         | IG1R_RAT | IG1R_MOUSE         | IRR RAT            | INSR AEDAE         | PPAP_HUMAN | IRS2_MOUSE | SFPO_HUMAN | MLL2_HUMAN         |
|           | DB             | -                  | -        |                    |            |            | -          |            |                    |                    |                    |            |            |            |            |            |                    | -          | -          | -          | -          | 7                  | -        | -                  | -         | ч                  | ч        | -                  | -                  | -                  | -          | Н          | -          | П                  |
|           | Length         | 1255               | 1257     | 1254               | 703        | 1210       | 1308       | 1210       | 1308               | 1342               | 1339               | 1167       | 1426       | 1367       | 1363       | 245        | 1477               | 2146       | 1382       | 1372       | 1607       | 1300               | 1383     | 1297               | 1300      | 1367               | 1370     | 1373               | 581                | 1390               | 386        | 1321       | 707        | 5262               |
|           | Query<br>Match | •                  | 4.5      |                    |            |            | 3.9        |            | 3.7                | 3.1                |                    |            | 7.7        |            | 0.5        |            | •                  | ٠          | ٠          | ٠          | ٠          | 8<br>.3            | •        | •                  | •         |                    | •        | ٠                  | ٠                  |                    | ٠          | •          | 0.0        | 0.9                |
| de        | A Q            | 7                  | Ò        | 64                 | Ñ          | 'n         | 23         | 'n         | ~                  | ~                  | 'n                 | ĸ          |            | H          | Ä          |            |                    | •          | _          | _          | _          | _                  | _        | _                  | _         | _                  | •        | •                  |                    | _                  |            |            |            |                    |
|           | Score          | 2405.5             | 1947.5   | 1935               | 755.5      | 721        | 721        | 717.5      | 717                | 697                | 668                | 655.5      | 536        | 404.5      | 317.5      | 293        | 273.5              | 270.5      | 256.5      | 252.5      | 252        | 251.5              | 249      | 248.5              | 246.5     | 246                | 235.5    | 233.5              | 228.5              | 207                | 168        | 155        | 151.5      | 151.5              |
|           | Result<br>No.  | -                  | 7        | m                  | 4          | ស          | 9          | 7          | හ                  | σ                  | 10                 | 11         | 12         | 13         | 14         | 15         | 16                 | 17         | 18         | 19         | 20         | 21                 | 22       | 23                 | 24        | 25                 | 56       | 27                 | 28                 | 29                 | 30         | 31         | 32         | 33                 |

| Q14162 homo sapien Q92793 homo sapien Q97787 homo sapien Q9115 branchiosto P00534 avian leuko Q96gp6 homo sapien Q1038 nycobacteri P13983 nicotiana t P04280 homo sapien O54951 mus musculu P54252 mus musculu |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| SREC HUMAN CBP HUMAN MII]—HUMAN MII]—HUMAN EXEZ HRACL ERBB—ALV EXEZ HUMAN ODO2 MYCTU EXTN TOBAC EXTN TOBAC EXTN TOBAC EXTN HUMAN SM6B—MOUSE DREL HUMAN SRC2_MOUSE                                              |
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| 830<br>2442<br>863<br>1696<br>634<br>870<br>553<br>620<br>331<br>1185                                                                                                                                          |
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| 141.5<br>141.5<br>140<br>140<br>139<br>139.5<br>137.5<br>133.5<br>131.5                                                                                                                                        |
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# ALIGNMENTS

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                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                      Vyosine phosphate.
Subunir: Heterodiamer with each of the other ERBB receptors
(Potential). Interacts with PRKCABP (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
FTM: Ligand-binding increases phosphorylation on tyrosine residues (By similarity).
POLYMORPHISM: There are fours alleles due to the variations in positions 654 and 655. Allele B1 (11e-654/Ile-655) has a frequency of 0.782; allele B2 (11e-654/Val-655) has a frequency of 0.206; allele B3 (Val-655) has a frequency of 0.206; SIMILARITY: Belongs to the EGF receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                          R GO; GO: 0005012; F:Neu/ErbB-2 receptor activity; TAS.
R GO; GO: 0004716; F:receptor signaling protein tyrosine kinase . . .;
R GO; GO: 0004716; F:receptor signaling protein tyrosine kinase . . .;
R GO; GO: 0004716; F:receptor signaling protein tyrosine kinase . . .;
R GO; GO: 0006470; P:early proliferation; TAS.
GO; GO: 0006468; P:protein amino acid dephosphorylation; TAS.
R InterPro; IPR006494; EREL L domain.
InterPro; IPR006419; Purin_Tike.
R InterPro; IPR006511; Purin_Tike.
R InterPro; IPR006512; Furin repeat.
R InterPro; IPR00199303 Grow_Eac_recep.
R InterPro; IPR001993 Grow_Eac_recep.
R InterPro; IPR00199; Prof. Kinase.
InterPro; IPR004019; Prof. Kinase.
InterPro; IPR004019; Yr_pkinase AS.
R InterPro; IPR00199; Yr_pkinase AS.
R Pfam; PR00109; PYRKINASE.
R Probom; PR00109; PYRKINASE.
R PROSITE; PS00109; PYRKINASE TYR; 1.
R PROSITE; PS00109; PROTEIN KINASE ATP; 1.
R PROSITE; PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
Polymorphism; 3D-structure.
   alpha and amphiregulin.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
PROTEIN KINASE.
ATP (BY SIMILARITY).
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PDB; 1QR1; 01-JAN-00.
Genew; HGNC:3430; ERBB2.
MIM; 164870; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.7%; Score 2405.5; DB 1; Length 1255; 41.1%; Pred. No. 1.6e-137; ive 0; Mismatches 3; Indels 727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW; 39E9DFDA04DCF962 CRC64;
ATP (BY SIMILARITY).
BY SIMILARITY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1255 AA; 137909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 41.1
Matches 509; Conservative
       1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1170
                                                                                                                                                                                                                                                                                                    511
515
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```

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

sw model OM protein - protein search, using September Run on:

9, 2004, 12:29:10; Search time 17.7175 Seconds (without alignments) 3013.200 Million cell updates/sec

US-09-821-883-1 3020 1. MRAAPLLLARAASLSLGFLF.......ENPEYLGLDVPAAAHHHHH 555

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | protein-tyrosine k | protein-tyrogine k | p-185 precursor - | epidermal growth f |        |       |        |        | epidermal growth f | М      | epidermal growth f. | _      |        | protein let-23 [im | protein-tyrosine k | protein-tyrosine k | epidermal growth f |        |        | epidermal growth f | epidermal growth f | insulin-like growt | protein-tyrosine k | insulin receptor ( | insulin receptor - | insulin receptor p | insulin receptor p | insulin-like growt | insulin receptor p |
|-----------|----------------|--------------------|--------------------|-------------------|--------------------|--------|-------|--------|--------|--------------------|--------|---------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ID             | A24571             | TVRTNU             | 148161            | TVCHLV             | A42032 | GOHUE | A47253 | A53183 | A36325             | A36223 | JC4387              | S06142 | A27131 | E88257             | S70712             | S70713             | GQFFE              | D45558 | A45558 | B45558             | C45558             | T43220             | T18534             | S57245             | A56081             | INHUR              | A34157             | T43212             | A36080             |
|           | DB             | : -                | -                  | ~                 | Н                  | ~      | Н     | ~      | 7      | ~                  | ~      | ~                   | -      | ~      | ~                  | ~                  | ~                  | -                  | ~      | -      | C3                 | ~                  | ~                  | ~                  | ~                  | Н                  | Н                  | N                  | ~                  | 0                  |
|           | Length         | 1255               | 1260               | 1254              | 1223               | 527    | 1210  | 1308   | 1210   | 644                | 1342   | 1339                | 1166   | 843    | 1323               | 1374               | 1369               | 1330               | 366    | 1717   | 333                | 342                | 1363               | 1477               | 2101               | 2148               | 1382               | 1372               | 1607               | 1383               |
| 4         | Query<br>Match | 7.67               | 64.6               | 64.1              | 25.0               | ď.     | •     | 23.9   |        |                    | 23.1   |                     | 21.7   | 17.7   | 13.4               | 13.4               | 12.9               | 12.4               | 11.3   | 11.3   |                    | 11.0               |                    | 9.1                |                    |                    | 9.5                |                    | 8.3                | 8.2                |
|           | Score          | 2405.5             | 1950.5             | 1935              | 755.5              | 754.5  | 721   | 721    | -      | 714.5              | 697    | 662                 | 655.5  | 536    | 404.5              | 404.5              | 390.5              | 375.5              | 341    | 341    | 331                |                    | 317.5              | 273.5              | 270.5              | 270.5              | 256.5              | 252.5              | 252                | 249                |
|           | Result<br>No.  | 1                  | 7                  | m                 | 4                  | ហ      | 9     | 7      | 80     | o                  | 10     | 11                  | 12     | 13     | 14                 | 15                 | 16                 | 17                 | 18     | 19     | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 | 56                 | 27                 | . 28               | 29                 |

| insulin receptor-r | ingulin-like growt | ingulin receptor-r | tyrosine kinase re | insulin-like growt | insulin receptor-r | insulin-like growt | insulin receptor - | ingulin receptor h | acid phosphatase ( | PTB-associated spl | ALR protein - huma | hypothetical prote | cell wall glycopro | hypothetical prote | hypothetical prote |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| A36502             | IGHUR1             | B47417             | JH0803             | A33837             | B36502             | A48805             | T30346             | T42047             | JH0610             | A46302             | T03454             | S50754             | S50062             | T29293             | 850755             |
| ~                  | Н                  | ~                  | ~                  | ~                  | N                  | ~                  | ~                  | ~                  | Н                  | 7                  | 7                  | 7                  | N                  | N                  | 0                  |
| 1300               | 1367               | 540                | 183                | 1371               | 1268               | 329                | 1390               | 1846               | 386                | 707                | 5262               | 351                | 442                | 309                | 473                |
| 8.2                | 8.1                | 7.9                | 7.8                | 7.8                | 7.7                | 7.4                | 6.9                | 6.2                | 5.6                | 5.0                | 5.0                | 4.8                | 4.8                | 4.7                | 4.6                |
| 246.5              | 246                | 238                | 235.5              | 235.5              | 231.5              | 223.5              | 207                | . 188              | 168                | 151.5              | 151.5              | 145.5              | 145.5              | 142.5              | 140                |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

# ALIGNMENTS

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RESULT 1 A24571 protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N:Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB

C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence\_revision 06-Dec-1996 #text\_change 11-Jun-1999
C;Date: 25-Oct-1987 #sequence\_revision 06-Dec-1996 #text\_change 11-Jun-1999
C;Accession: AAS471; AA2481; A44188; B44188; IS9509; IS7622
R;Yamamoto, T.; Ikawa, S; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.;
Nature 319, 230-234, 1986
A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth £
A;Reference number: A24571; MUID:86118663; PMID:3003577

A; Accession: A24571

A;Molecule type: mRNA A;Residues: 1-1255 <YAM> A;Residues: 1-1255 <YAM> A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198 B;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985 A;Title: A v-erbb-related protooncogene, c-erbb-2, is distinct from the c-erbB-1/epiderm A;Reference number: A25491; WUID:86016729; PMID:2995967

J.; Seeburg, P A;Molecule type: DNA A;Residues: 737-1031 <SEM> A;Cross-references: GB:M1767; NID:g182163; PIDN:AAA35808.1; PID:g553282 A;Crossens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, Science 230, 1132-1139, 1985

A,Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromos A,Reference number: A44188; MUID:86070181; PMID:2999974

A;Accession: A44188

A,Molecule type: DNA A,Residues: 740-910 <COU1> A,Croserreferonces: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A,Accession: B44188

A; Molecule type: mRNA

A;Residues: 1-517, RALL', 522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2>
A;Cross-references: GB:M11730; NID:g183986
R;King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A;Reference number: 159509; MUID:85272597; PMID:2992089
A;Accession: 159509

A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
A;Title: Human HER2 (neu)
A;Reference number: IS7622; MUID:87286898; PMID:3039351

A; Status: translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1-191 <TAL>

Mon Sep 13 07:41:00 2004

|                                                                                                                                                                                                                                          | Db 616 FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVLGVVFGILI 675                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1                                                                                                                                                                                                                                        | Qy 330 329                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| ;Gene: GDB:ERBB2; NGL; NEU; HER-2;Cross-references: GDB:120613; OMIM:164870                                                                                                                                                              | DD 676 KRRQQKIRKYTWRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 735                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| Map position: 17q21.1-17q21.1<br>Introns: 25/1; 75/3; 147/1; 883/3                                                                                                                                                                       | Qy 330 329                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| Note: the list of introns is incomplete; Function:                                                                                                                                                                                       | Db 736 KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDBAYVMAGVGSPYVSRLLGICLTSTVQ 795                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| bescription: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP; superfamily: epidermal growth factor receptor; protein kinase homology                                                                                 | Qy 330 329                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| ;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho<br>nase                                                                                                                                          | Db 796 LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS 855                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| ;1-21/Domain: signal sequence #status predicted <sig><br/>;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <mat></mat></sig>                                                                                            | Qy 330 329                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| ;22-653/Domain: extracellular #status predicted <ext><br/>;70-304/Domain: EGF receptor extracellular domain repeat <ee1></ee1></ext>                                                                                                     | Db 856 PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 915                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| ;395-605/Domain: EGF receptor extracellular domain repeat <ee2><br/>;654-675/Domain: transmembrane #status predicted <twm></twm></ee2>                                                                                                   | Qy 330 329                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| ,676-1255/Domain: intracellular #status predicted <int><br/>,718-983/Domain: protein kinase homology <kin></kin></int>                                                                                                                   | DD 916 MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE 975                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| F;726-734/Region: protein kinase ATP-binding motti<br>F;68,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predict<br>F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ;753/Active site: Lys #status predicted<br>;1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)                                                                                                        | 9/6 FSKMAKUPÇKEVVIQNBULGFAGFIDSIFIKASILIBDUKADUKADUKALIVEÇKALICET FOL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| Query Match 79.7%; Score 2405.5; DB 1; Length 1255; Beet Local Similarity 41.1%; Pred. No. 3.7e-133;                                                                                                                                     | OY 330 - GAGGWAHTRIANSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA 1095                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| ; Conservative 0; Mismatches 3; Indels 727; Gaps                                                                                                                                                                                         | Qy 388 KGLQSLPTHDPSPLQRYSEDPTVPLPSRTDGYVAPLTCSPQPBYVNQPDVRPQPPSPREG 447                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| Qy 35 LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYGGCQVVQGNLELTYLPTNNSLSFLQ 94                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| . +                                                                                                                                                                                                                                      | QY 448 PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP 507<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| Н                                                                                                                                                                                                                                        | Qy 508 AFDNLYYWDQDPPERCAPPSTFKGTPTAENPEYLGLDVP 546                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Qy 155 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC 214                                                                                                                                                                  | Db 1216 AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 1254                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 215 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC 27                                                                                                                                                                      | RESULT 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| 196 SPWCKGSRCWGESSEDCQSLTRIVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC                                                                                                                                                                         | orecursor - rat                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCYTACPYNYLSTDVGS 32                                                                                                                                                                               | C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999<br>C;Accession: A24562; A61204                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| 256 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC 31                                                                                                                                                                      | Ridargmann, C.1.; Hung, M.C.; Weinberg, K.A. Ridure 319, 226-230, 1986 North and Company of American and Amer |
| Qy 330                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 330                                                                                                                                                                                                                                      | A;Molecule type: mRNA<br>A;Residues: 1-1260 <bar></bar>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|                                                                                                                                                                                                                                          | A;Cross-references: EMBL:X03362; NID:g56745; PIDN:CAAZ/U59.1; FIL:g56746 R;Masui, T: Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Qy 330 329                                                                                                                                                                                                                               | Carcinogenesis 12, 19/3-19/8, 1991<br>A,Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no m<br>2.+his-olvilformanide or N-methyl-N-nitrosourea.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Db 436 LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 495                                                                                                                                                                  | A; Reference number: A61204; MUID:92035293; PMID:1682063<br>A. Accession: A61204                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Qy 330 329                                                                                                                                                                                                                               | A;Status: preliminary<br>A:Molecule type: DNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| Db 496 TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV 555                                                                                                                                                                  | A;Residues: 637-663,'V',665-702 <mas><br/>A;Note: authors translated the codon GCA for residue 25 as Val</mas>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Qy 330 329                                                                                                                                                                                                                               | C;Genetics:<br>A;Gene: neu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| DD 556 NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615                                                                                                                                                                  | C;Superfamily: epidermal growth factor receptor; protein kinase homology<br>C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| Ov 330 329                                                                                                                                                                                                                               | Fil-19/Domain: signal sequence #status predicted                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |





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1 MRAAPLLLARAASLSLGFLF.......ENPEYLGLDVPAAAHHHHH 555
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUBL.pep:*

3: /cgn2_6/ptodata/2/pubpaa/SCT_NEW PUBL.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1335176
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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DB seq length: 200000000
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Perfect score:
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Maximum I
                                                                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description                   | Sequence 1, Appli | Sequence 3, Appli | Sequence 2, Appli | Sequence 4, Appli | Sequence 6, Appli | Sequence 9, Appli | Sequence 3, Appli | 7               | Sequence 4, Appli | Sequence 126, App | Sequence 6, Appli | ς,              | 4               | Sequence 28, Appl | Sequence 594, App |
|-------------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-------------------|-------------------|-------------------|-----------------|-----------------|-------------------|-------------------|
| ID                            | US-09-821-883-1   | US-09-821-883-3   | US-09-821-883-2   | US-09-821-883-4   | US-09-854-356-6   | US-09-811-123-9   | US-09-811-115-3   | US-09-769-508-2 | US-09-984-092-4   | US-10-177-293-126 | US-10-207-498-6   | US-10-338-730-2 | US-10-322-892-4 | US-10-272-437A-28 | US-10-117-937-594 |
| DB                            | 6                 | σ                 | σ                 | 0                 | 0                 | 6                 | 6                 | 6               | 12                | 14                | 14                | 14              | 14              | 15                | 15                |
| %<br>Query<br>Watch Length DB | 555               | 564               | 69                | 697               | 919               | 1255              | 1255              | 1255            | 1255              | 1255              | 1255              | 1255            | 1255            | 1255              | 1255              |
| &<br>Ouery<br>Match           | 100.0             | 99.5              | 98.4              | 97.9              | 85.2              | 79.8              | 79.8              | 79.8            | 79.8              | 79.8              | 79.8              | 79.8            | 79.8            | 79.8              | 79.8              |
| Score                         | 3020              | 3005.5            | 2972              | 2957.5            | 2573.5            | 2410.5            | 2410.5            | 2410.5          | 2410.5            | 2410.5            | 2410.5            | 2410.5          | 2410.5          | 2410.5            | 2410.5            |
| Result<br>No.                 | -                 | 7                 | m                 | 4                 | S                 | 9                 | 7                 | ω               | 6                 | 10                | 11                | 12              | 13              | 14                | 15                |

61 HLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRI 120

8 8 8

61 HEDMERHLYQGCQVVQGNEELTYLPTNASESFLQDIQEVQGYVLIAHNQVRQVPLQRERI

121 VRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQL 180

| Sequence 36, Appl Sequence 126, App Sequence 1, Appl Sequence 2, Appl Sequence 3, Appl Sequence 3, Appl Sequence 53, Appl Sequence 53, Appl Sequence 45, Appl Sequence 45, Appl Sequence 68, Appl Sequence 68, Appl Sequence 14, Appl Sequence 14, Appl Sequence 118, Appl Sequence 13, Appl Sequence 14, Appl Sequence 14, Appl Sequence 13, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 11, Appl Sequence | Dendritic                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Length 555; Indels 0; Gaps 0; TQVCTGTDMKLRLPASPET 60                                                                                                                                                        |
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| 1255 15 US-10-435-696-36 1255 16 US-10-744-779C-4 1255 9 US-09-854-126 1255 9 US-09-864-126 1255 10 US-09-930-125-2 1255 12 US-10-418-141-6 1255 12 US-10-459-162-3 1255 12 US-10-459-162-3 1255 12 US-10-23-286-553 1255 12 US-10-313-644-2 1255 14 US-10-313-644-2 1255 15 US-10-313-644-2 1255 15 US-10-313-644-2 1255 15 US-10-149-138-4641 1255 16 US-10-149-138-4641 1255 16 US-10-149-138-4641 1255 16 US-10-149-138-4641 1255 16 US-10-149-138-4641 1256 9 US-09-874-89-18 1256 9 US-09-874-89-18 1256 9 US-09-81-83-5 1257 US-09-81-83-5 1258 9 US-09-81-83-5 1258 9 US-09-81-83-5 1259 US-09-81-83-5 1259 US-09-81-83-5 1259 US-09-81-83-5 1259 US-09-84-35-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ALIGNMENTS and Methods for Immunotherapy 9/821,883 193,504 rsion 4.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | <pre>imilarity 100.0%; Score 3020; DB 9; Length 555;  conservative 0; Mismatches 0; Indels 0; Gaps  MRAAPLILARAASLSLGFLFLLFFWLDRSVLAKELARGAASTQVCTGTDMKLRLPASPET                                     </pre> |
| 16 2410.5 79.8 119 2410.5 79.8 119 2410.5 79.8 119 2410.5 79.8 119 2410.5 579.8 119 2405.5 79.7 112 22 2405.5 79.7 112 2405.5 79.7 112 2405.5 79.7 112 2405.5 79.7 112 2405.5 79.7 113 2405.5 79.7 113 2405.5 79.7 113 2405.5 79.7 114 24 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 44 11612 53.4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | RESULT 1 US-09-821-883-1 Sequence 1, Application US/098218; BATEAL NO. US2020061310A1 GENERAL INFORMATION: APPLICANT: Vidovic, Damir APPLICANT: Vidovic, Damir APPLICANT: Graddis, Thomas TITLE OF INVENTION: Compositions; FILE REFERENCE: 7636-0022.30 CURRENT PILING DATE: 2001-03-30; CURRENT PILING DATE: 2000-03-30; PRIOR APPLICATION NUMBER: US 60/; PRIOR FILING DATE: 2000-03-30; NUMBER OF SEQ ID NOS: 30 SOFTWARE: FASESEQ for Windows Ve; SEQ ID NO 1 LENGTH: 555 TYPE: BRT ORGANISM: Artificial Sequence FEATURE: CTHER INFORMATION: HERSOO CONSCIUS- | Ouery Match Best Local Similarity 100 Matches 555, Conservative Oy 1 MRAAPLLLARAASLS Db 1 MRAAPLLLARAASLS                                                                                                   |

300

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531

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MPNPEGRYTFGASCVTACPYNYLSTDVGS-----GAGGMVHHRHRSSSTRSGGGDL 351
                                                                                                                                                                                                                 TIGLEPSEEERPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 420
                                                                                                                                                                                                                                                       LPSETDGYVAPLICSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNG 471
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                  CYODILLWKDIFHKNNOLALTLIDTNRSRACHPCSPWCKGSRCWGESSEDCOSLTRTVCA
                                                               GGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFES
                                                                               TLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP
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 CYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA
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APPLICANT: Laus, Reiner
APPLICANT: Uddovic, Damir
APPLICANT: Uddovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Coll-Based Immuncherapy
FILE REPERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
FRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 690;
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98.4%; Score 2972; DB 9; I
Best Local Similarity 100.0%; Pred. No. 1.4e-199;
Matches 549; Conservative 0; Mismatches 0;
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Patent No. US20020061310A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                   CYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA
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Sequence 3, Application US/09821883
Sequence 3, Application US/09821883
GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Uddovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 564
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US-09-821-883-3
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Best Local Similarity 98.4%;
Matches 555; Conservative
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September 9, 2004, 12:20:15; Search time 61.1253 Seconds (without alignments) 2565.449 Million cell updates/sec
5.1.6
Compugen Ltd.
version 5
                                                            - protein search, using sw model
GenCore (c) 1993 -
               Copyright
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3020 1 MRAAPLLLARAASLSLGFLF......ENPEYLGLDVPAAHHHHH 555 US-09-821-883-1 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB @ Maximum DB @

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A Geneseq 29Jan04:\* **Database** :

geneseqp1980s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003as:\* geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Description                | Aae1310 | Aae13110 Human HER | Aae13109 Human HER | Aael3111 Human HER | Aab21203 Human HER | Aam51148 Her-2/neu | Aay92620 Human her | 7        | Aae12130 Human tyr | Aae26349 Human HER | Aae26366 Human Her | Aau74545 Human HER | Abr47447 Breast ca | Abp74708 Human Her | Aae38390 Human c-e |          | Ada37255 Human Erb | Adb67621 Human epi | Aaw01111 HER-2/neu | Aaw92406 Human HER | Aay84780 Amino aci | Aab21198 Human HER | Aag88267 HER2/neu | Aab85458 Human HER | Aae20479 Human Her |
|----------------------------|---------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|
| αı                         | 1310    | AAE13110           | AAE13109           | AAE13111           | AAB21203           | AAM51148           | AAY92620           | AAB60167 | AAE12130           | AAE26349           | AAE26366           | AAU74545           | ABR47447           | ABP74708           | AAE38390           | ADA38143 | ADA37255           | ADB67621           | AAW01111           | AAW92406           | AAY84780           | AAB21198           | AAG88267          | AAB85458           | AAE20479           |
| DB                         | 4       | 4                  | 4                  | 4                  | m                  | S                  | ო                  | 4        | 4                  | s                  | S                  | S                  | ø                  | 9                  | 9                  | 9        | ^                  | ^                  | ~                  | ~                  | m                  | m                  | 4                 | 4                  | 5                  |
| %<br>Query<br>Match Length | 55      | 564                | 069                | 697                | 919                | 919                | 1255               | 1255     | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255     | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255              | 1255               | 1255               |
| Query<br>Match             | 0       | 99.5               | 98.4               | 97.9               | 85.2               | 85.2               | 79.8               | 79.8     | •                  | 79.8               | 79.8               | 79.8               | 79.8               | 79.8               | 79.8               | 79.8     | 79.8               | 79.8               | 79.7               | 79.7               | 79.7               | 79.7               | 79.7              | 79.7               | 79.7               |
| Score                      | 30      | 3005.5             | 2972               | 2957.5             |                    |                    | 2410.5             | 2410.5   | 410.               | 2410.5             | 2410.5             |                    | 2410.5             | 2410.5             |                    | 2410.5   | 2410.5             | 2410.5             | 2405.5             | 2405.5             | 2405.5             | 2405.5             | 405.              | 2405.5             | 2405.5             |
| Result<br>No.              |         | ~                  | m                  | 4                  | S                  | 9                  | 7                  | œ        | 6                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16       | 17                 | 18                 | 19                 |                    |                    | 22                 |                   | 24                 | 25                 |

| Aau77114 Human Her | Aam51143 Human Her | Aae24067 Human Her | Abr43687 Human c-e | Abr82066 Human Her | Adc09593 Her2/Neu | Add25484 Binding d | Ade63281 Human Pro |          | Adc35106 Human bre | Aar39568 Sequence | Aau98923 Human bre | Aam51152 Mouse Her | Aam51153 Mouse Her | Aab21208 Human HER | Aab21206 Mouse Her | Aag62860 Amino aci | Aam51151 Mouse Her | Abu79135 ErbB2 (HE | Aab21199 Rat HER-2 |
|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|----------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AAU77114           | AAM51143           | AAE24067           | ABR43687           | ABR82066           | ADC09593          | ADD25484           | ADE63281           | ADE76190 | ADC35106           | AAR39568          | AAU98923           | AAM51152           | AAM51153           | AAB21208           | AAB21206           | AAG62860           | AAM51151           | ABU79135           | AAB21199           |
| 1255 5             | 1255 5             | 1255 5             | 1255 6             | 1255 7             | 1255 7            | 1255 7             | 1255 7             | 1255 7   | 1253 7             | 1433 2            | 1223 5             | 920 5              | 926 5              | 1200 3             | 1256 3             | 1256 4             | 1256 5             | 1260 6             | 1256 3             |
| 79.7               | 79.7               | 79.7               | 79.7               | 79.7               | 79.7              | 79.7               | 79.7               | 79.7     | 79.4               | 79.1              | 77.3               | 70.5               | 70.5               | 69.3               | 64.9               | 64.9               | 64.9               | 64.6               | 64.5               |
| 2405.5             | 2405.5             | 2405.5             | 2405.5             | 2405.5             | 2405.5            | 2405.5             | 2405.5             | 2405.5   | 2398.5             | 2389.5            | 2334.5             | 2129               | 2129               | 2092.5             | 1961               | 1961               | 1961               | 1950.5             | 1948               |
| 56                 | 27                 | 28                 | 29                 | 30                 | 31                | 32                 | 33                 | 34       | 35                 | 36                | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

Human HER500 fusion protein construct. AAE13108 standard; protein; 555 AA 28-JAN-2002 (first entry) AAE13108; AAE13108 

Immunostimulatory fusion protein; IFP; antigen component; therapy; immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoms; ovarian cancer; PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal tag; human; HER-2 protein; HER500 fusion protein.

WO200174855-A2. Homo sapiens. 11-OCT-2001. Synthetic. Chimeric.

30-MAR-2001; 2001WO-US010515. 30-MAR-2000; 2000US-0193504P.

Graddis T; (DEND-) DENDREON CORP. Laus R, Vidovic D,

WPI; 2001-662965/76. N-PSDB; AAD21564.

An immunostimulatory fusion protein comprising the intracellular domain of HER-2 and an antigen elicits an immune response to the antigen and is useful for the treatment of associated cancer associated.

Claim 7; Page 26; 59pp; English.

The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (CD) induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are

WO200174855-A2.

Chimeric

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used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular and intracellular domains an
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100.0%; Pred. No. 6.4
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fusion protein construct comprising OVA-derived octapeptide
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                                  Ź
                                  AAE13110 standard; protein; 564
                                                                                                   (first entry)
                                                                                                                                     Human HER500
                                                                                                                                                                                                                                                                                              Homo sapiens
Unidentified
                                                                                                     28-JAN-2002
                                                                  AAE13110;
RESULT
AAE1311
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420

TLGLEPSEEEBAPRSPLAPSECAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP

LPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLBRAKTLSPGKNG

TLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP

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nucleic acid molecules encoding such proteins. The IPPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC) induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer suscito with a particularly antigen. The present sequence is HER500 fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular domain, an Ala linker, an intracellular domain and a C-terminal tag
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                                                                                                                                                                                                                                            An immunostimulatory fusion protein comprising the intracellular domain of HER-2 and an antigen elicits an immune response to the antigen and is useful for the treatment of associated cancer associated.
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Pred. No. 6.7e-201;
0; Mismatches 0;
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                                                                                                                                                                      Graddis T;
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98.4%;
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N-PSDB; AAD21566.
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